

Qy	2	VTLDESGGGLQTPGGALSLVCKASGFTTFSHGMMWVRQTPKGLWVAGISNTGTYTYA	61
Db	2	VQLVESGGGLVQPGGSLRLSCAASGFTTFSVAMSWVRQAPKGLWYSALSGSGSTYYA	61
Qy	62	PAVKGRATISRDNQGQSTVRLQLNNLRADFTGTYTCAKGAYCAGCGGIDAWGHGTEIV	121
Db	62	DSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYYCARSSPMYEG--FDLWGGQGLTVT	119
Qy	122	SS 123	
Db	120	SS 121	

[illegible]

```

QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAKGGAYCAGCGGIDAWGHGTEVIV 121
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 62 DSVKGRFTISRDNKNTLYLQMNTRAEADTAVYICARRASY-----DYWGQGTWTVV 113
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 122 SS 123
      ||
Db 114 SS 115

```

```

RESULT 6
US-10-291-265-427
; Sequence 427, Application US/10291265
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-427

```

```

Query Match 57.5%; Score 381; DB 6; Length 313;
Best Local Similarity 62.7%; Pred. No. 3.9e-23;
Matches 79; Conservative 11; Mismatches 32; Indels 4; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMWVRQTPGKGLEWVAGISNTGYTYA 61
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 62 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAGISGGSSTYY 121
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAGK--GAY--CAGCGGIDAWGHGT 117
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 122 DSVKGRFTISRDNKNTLYLQMNTRAEADTAVYICAKSHPGYIYDSSGYSYFYDIWGQGT 181
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 118 EVIVSS 123
      |||
Db 182 LTVSS 187

```

```

RESULT 7
US-10-291-265-804
; Sequence 804, Application US/10291265
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0

```

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; SEQ ID NO 804
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-804

```

```

Query Match 57.2%; Score 379.5; DB 6; Length 384;
Best Local Similarity 57.8%; Pred. No. 6.1e-23;
Matches 78; Conservative 12; Mismatches 32; Indels 13; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMWVRQTPGKGLEWVAGISNT-GTYTY 60
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 21 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAGISGGSSTYY 80
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 61 PAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAKGGAYCAGCGG----- 109
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 81 ADSVKGRFTISRDNKNTLYLQMNTRAEADTARYCAKGGVELASTKPPSSIRLNPIRYW 140
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 110 -IDAWGHGTEVIVSS 123
      |||
Db 141 YFDLWGQGTLLTVSS 155

```

```

RESULT 8
US-10-291-265-805
; Sequence 805, Application US/10291265
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

```

```

Query Match 57.2%; Score 379.5; DB 6; Length 384;
Best Local Similarity 57.8%; Pred. No. 6.1e-23;
Matches 78; Conservative 12; Mismatches 32; Indels 13; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMWVRQTPGKGLEWVAGISNT-GTYTY 60
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 21 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAGISGGSSTYY 80
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 61 PAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAKGGAYCAGCGG----- 109
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 81 ADSVKGRFTISRDNKNTLYLQMNTRAEADTARYCAKGGVELASTKPPSSIRLNPIRYW 140
      :||||| :||||| :||:| :||||| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 110 -IDAWGHGTEVIVSS 123
      |||
Db 141 YFDLWGQGTLLTVSS 155

```

```

RESULT 9
US-10-291-265-806
; Sequence 806, Application US/10291265
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

```

FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 806
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-10-291-265-806

Query Match 57.2%; Score 379.5; DB 6; Length 384;
Best Local Similarity 57.8%; Pred. No. 6.1e-23;
Matches 78; Conservative 12; Mismatches 32; Indels 13; Gaps 2;
QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSSHGMMWVRQTPGKLEWVAGISNT-GTYTY 60
DB 21 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGLSGSGSSTYY 80
QY 61 APVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGKGYACGCGD----- 109
DB 81 ADSVKGRTISRDNKNTLYLQMNLSRADDTARYYCAKGGVELASTKPSIWRLNPIRYW 140
QY 110 -IDAWGHGTEVIVSS 123
DB 141 YFDLWGGTGLTVSS 155

RESULT 10
US-10-291-265-807
Sequence 807, Application US/10291265
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 807
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-10-291-265-807

Query Match 57.2%; Score 379.5; DB 6; Length 384;
Best Local Similarity 57.8%; Pred. No. 6.1e-23;
Matches 78; Conservative 12; Mismatches 32; Indels 13; Gaps 2;
QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSSHGMMWVRQTPGKLEWVAGISNT-GTYTY 60
DB 21 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGLSGSGSSTYY 80
QY 61 APVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGKGYACGCGD----- 109
DB 81 ADSVKGRTISRDNKNTLYLQMNLSRADDTARYYCAKGGVELASTKPSIWRLNPIRYW 140

QY 110 -IDAWGHGTEVIVSS 123
DB 141 YFDLWGGTGLTVSS 155
RESULT 11
US-09-723-752B-11
Sequence 11, Application US/09723752B
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,752B
FILING DATE: 27-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: PI093P1DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-723-752B-11

Query Match 57.0%; Score 378; DB 5; Length 113;
Best Local Similarity 62.3%; Pred. No. 2.7e-23;
Matches 76; Conservative 10; Mismatches 26; Indels 10; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGYTYA 61
DB 2 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGLSGSGSSTYYA 61
QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGKGYACGCGDIDAWGHGTEVIV 121
DB 62 DSVKGRFTISRDNKNTLYLQMNLSRADDTARYYCAARG-----FDYWGQGTGLTV 111
QY 122 SS 123
DB 112 SS 113

RESULT 12
PCT-US03-21304-56
Sequence 56, Application PC/TUS0321304


```

RESULT 13
US-10-602-727-50
; Sequence 50, Application US/10602727
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies Against Protective Antigen
; FILE REFERENCE: PF596Pin
; CURRENT APPLICATION NUMBER: US/10/602,727
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/391,162
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/406,339
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/417,305
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/426,360
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/434,807
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/438,004
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/443,858
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/443,781
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/454,613
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/468,651
; PRIOR FILING DATE: 2003-03-08
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PWD0283 scfV

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```

RESULT 15
US-10-600-152-15
; Sequence 15, Application US/10600152
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/10/600,152
; CURRENT FILING DATE: 2003-06-20

```

; PRIOR APPLICATION NUMBER: 09/648,067
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 60/151,018
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: US 60/213,822
 ; PRIOR FILING DATE: 2000-06-23
 ; NUMBER OF SEQ ID NOS: 15
 ; SEQ ID NO 15
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: VH consensus sequence
 US-10-600-152-15

Query Match
 Best Local Similarity 56.7%; Score 376; DB 6; Length 119;
 Matches 78; Conservative 10; Mismatches 29; Indels 6; Gaps 2;
 QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGTYTVA 61
 Db 2 VLVESGGGLVPGGSLRLSLSAASGFTFSSYAMSWVRQAPGKLEWVAVISGGGTYVA 61
 QY 62 PAVKGRATISRDNQSTVRLQLNNLRADTGTYCAKGCAYCAGCGDI-DAWGHGTEVI 120
 Db 62 DSVKGRFTISRDNKNTLYLQMNLSLRADTAVYYCARGV-----GYSLYDWGQGLT 116
 QY 121 VSS 123
 Db 117 VSS 119

Search completed: September 3, 2003, 12:54:36
 Job time : 9.10781 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	541	81.6		585	2	A46507	Ig alpha chain - c
2	522	78.7		138	2	A33334	Ig heavy chain pre
3	475.5	71.7		342	2	A46529	Ig gamma chain (5.
4	475.5	71.7		572	2	B46529	Ig y heavy chain (
5	394	59.4		119	2	C36005	Ig heavy chain v r
6	387.5	58.4		141	2	S31669	Ig heavy chain v r
7	386	58.2		123	2	S31114	Ig heavy chain - h
8	385	58.1		140	2	S31686	Ig heavy chain v r
9	383.5	57.8		120	2	S46798	Ig heavy chain v r
10	383	57.8		119	2	S31107	Ig heavy chain - h
11	381	57.5		119	2	S31108	Ig heavy chain - h
12	380.5	57.4		147	2	I37780	Ig variable region
13	380	57.3		146	2	I47196	Ig heavy chain var
14	378	57.0		134	2	S31699	Ig heavy chain v r
15	378	57.0		160	2	S05271	Ig heavy chain pre
16	377	56.9		138	2	S31666	Ig heavy chain v r
17	376	56.7		121	2	S19666	Ig heavy chain v r
18	375.5	56.6		145	2	I47185	Ig heavy chain v r
19	375	56.6		117	2	S78486	Ig heavy chain var
20	375	56.6		121	2	S56673	Ig heavy chain v r
21	372.5	56.2		118	2	S31116	Ig heavy chain - h
22	372.5	56.2		136	2	S31587	Ig heavy chain v r
23	372	56.1		119	2	D36005	Ig heavy chain v r
24	372	56.1		127	2	S38489	Ig heavy chain - h
25	372	56.1		140	2	I47204	Ig heavy chain var
26	371.5	56.0		128	2	S26790	Ig heavy chain v r
27	371.5	56.0		128	2	S26786	Ig heavy chain v r
28	371.5	56.0		145	2	I47203	Ig heavy chain var
29	371	56.0		152	2	B26471	Ig heavy chain pre

A:Title: Structural relationship between the two Igy of the duck, *Anas platyrhynchos*: md
 A:Reference number: A46529; MUID:93017865; PMID:1401901
 A:Accession: B46529
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-572 <MAG>

Query Match	59.4%	Score 394;	DB 2;	Length 119;
Best Local Similarity	64.8%	Pred. No. 2.3e-27;		
Matches	79;	Conservative 10;	Mismatches 29;	Indels 4; Gaps 1
Qy	2	VTLDESGGGTQTPGALSLVCKASGFTFSHHMMWVROT	PGKLEWVAGISNTGTYTYA	61
Db	2	VQLESGGGVLQPGGSLRLSCAASGFTFSVAMSVRQAP	KGKLEWVSAISGSGGTYA	61
Qy	62	PAVKGRATISRDNCGOSTVRQLNLNRADTGTYTCAGK	GCAGCGGIDAWHGTEVIV	121
Db	62	DSVKGRFTISRDNKNTFLYLQMSLRADTAIVYCAKD	-----AGWGSGFDYWGQGLTVV	117
Qy	122	SS 123		
Db	118	SS 119		

RESULT 6
S31669
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31669

R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31669
A:Status: preliminary
A:Molecule type: mRNA

A;Residues: 1-141 <CUI>

A;Cross-references: EMBL:Z14212; NID:g30959; PIDN:CAA78581.1; PID:g30960
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 387.5; DB 2; Length 141;
Best Local Similarity 62.3%; Pred. No. 9.7e-27;
Matches 76; Conservative 15; Mismatches 30; Indels 1; Gaps 1;

QY 2 VTLDSEGGGLQTPGGGALSIVCKASGFTFSSHGMWVRQTPGKLEWVAGISNTGYTYA 61
DB 21 VQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSAISGSGSTYYA 80

QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAGYACAGCGGDDAWGHGTEVIV 121
DB 81 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR-GRHLTGEKGFEDLWGRGTLTV 139

QY 122 SS 123
DB 140 SS 141

RESULT 7

S31114
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31114
R;Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <RAA>
A;Cross-references: EMBL:X62963
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 386; DB 2; Length 123;
Best Local Similarity 63.1%; Pred. No. 1.1e-26;
Matches 77; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 2 VTLDSEGGGLQTPGGGALSIVCKASGFTFSSHGMWVRQTPGKLEWVAGISNTGYTYA 61
DB 2 VQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAGYACAGCGGDDAWGHGTEVIV 121
DB 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARSLYRLFLEWLFYWGQGTLLTV 121

QY 122 SS 123
DB 122 SS 123

RESULT 8

S31686
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31686
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.1%; Score 385; DB 2; Length 140;
Best Local Similarity 62.9%; Pred. No. 1.6e-26;
Matches 78; Conservative 11; Mismatches 29; Indels 6; Gaps 2;

QY 2 VTLDSEGGGLQTPGGGALSIVCKASGFTFSSHGMWVRQTPGKLEWVAGISNTGYTYA 61
DB 21 VQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSAISGSGSTYYA 80

QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAGYACAGCGG--DIDAWGHGTEV 119
DB 81 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK----CFPAGSPSPFDYWGQGTLLV 136

QY 120 IVSS 123
DB 137 TVSS 140

RESULT 9

S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S48798
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies
A;Reference number: S48797
A;Accession: S48798
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <MAH>
A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.8%; Score 383.5; DB 2; Length 120;
Best Local Similarity 63.1%; Pred. No. 1.8e-26;
Matches 77; Conservative 12; Mismatches 30; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGGALSIVCKASGFTFSSHGMWVRQTPGKLEWVAGISNTGYTYA 61
DB 2 VQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAGYACAGCGGDDAWGHGTEVIV 121
DB 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDRGFWSYK---DYWGQGTLLTV 118

QY 122 SS 123
DB 119 SS 120

RESULT 10

S31107
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31107
R;Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>

C; Superfamily: immunoglobulin V region; immunoglobulin homology

Search completed: September 3, 2003, 12:16:29
Job time : 10.5703 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:01:44 ; Search time 5.65885 Seconds
(without alignments)
1022.165 Million cell updates/sec

Title: US-10-083-424A-18
Perfect score: 663
Sequence: 1 AVTLDESGGLQTPGGALSL.....AGCGGDIDAWGHGTIVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	349	52.6	115	1 HV32_MOUSE	P01801 mus musculus
2	347.5	52.4	126	1 HV3K_HUMAN	P01772 homo sapien
3	346	52.2	117	1 HV3C_HUMAN	P01764 homo sapien
4	344.5	52.0	136	1 HV16_MOUSE	P01783 mus musculus
5	342.5	51.7	111	1 HV35_MOUSE	P01804 mus musculus
6	342	51.6	113	1 HV27_MOUSE	P01796 mus musculus
7	340.5	51.4	122	1 HV3G_HUMAN	P01768 homo sapien
8	340	51.3	113	1 HV28_MOUSE	P01797 mus musculus
9	338	51.0	115	1 HV33_MOUSE	P01802 mus musculus
10	338	51.0	117	1 HV02_CANFA	P01785 canis famil
11	337	50.8	113	1 HV30_MOUSE	P01799 mus musculus
12	335.5	50.6	114	1 HV3B_HUMAN	P01763 homo sapien
13	335	50.5	113	1 HV29_MOUSE	P01798 mus musculus
14	333.5	50.3	122	1 HV3H_HUMAN	P01769 homo sapien
15	333	50.2	113	1 HV31_MOUSE	P01800 mus musculus
16	330	49.8	115	1 HV3F_HUMAN	P01767 homo sapien
17	329	49.6	121	1 HV3J_HUMAN	P01771 homo sapien
18	328	49.5	142	1 HV01_RAT	P01805 rattus norv
19	325.5	49.1	116	1 HV3T_HUMAN	P01781 homo sapien
20	324	48.9	115	1 HV3D_HUMAN	P01765 homo sapien
21	322	48.6	144	1 HV26_MOUSE	P01795 mus musculus
22	321.5	48.5	119	1 HV38_MOUSE	P01808 mus musculus
23	320	48.3	98	1 HV57_MOUSE	P18528 mus musculus
24	320	48.3	113	1 HV34_MOUSE	P01803 mus musculus
25	318.5	48.0	116	1 HV05_CARAU	P19181 carassius a
26	317	47.8	117	1 HV58_MOUSE	P18529 mus musculus
27	316	47.7	117	1 HV54_MOUSE	P18525 mus musculus
28	316	47.7	117	1 HV59_MOUSE	P18530 mus musculus
29	315.5	47.6	122	1 HV3A_HUMAN	P01762 homo sapien
30	313.5	47.3	97	1 HV56_MOUSE	P18527 mus musculus
31	313.5	47.3	120	1 HV30_HUMAN	P01782 homo sapien
32	313	47.2	123	1 HV24_MOUSE	P01793 mus musculus
33	312	47.1	117	1 HV55_MOUSE	P18526 mus musculus

ALIGNMENTS

RESULT 1									
ID	HV32_MOUSE								
AC	P01801:								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DE	15-SEP-2003 (Rel. 42, Last annotation update)								
OS	Ig heavy chain V-III region J606.								
OC	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE.								
RX	MEDLINE=8209361; PubMed=6798111;								
RA	Johnson N., Slankard J., Paul L., Hood L.;								
RT	"the complete V domain amino acid sequences of two myeloma inulin-								
RT	binding proteins.";								
RL	J. Immunol. 128:302-307(1982).								
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT								
CC	BINDS INULIN.								
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.								
DR	PIR; C92811; AVMS06.								
DR	HSP; P01789; IMCP.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003006; Ig_MHC.								
DR	InterPro; IPR003596; Ig_V.								
DR	Pfam; PF00047; Ig_1.								
DR	SMART; SM00406; IGV; 1.								
DR	PROSITE; PS00835; IG_LIKE; 1.								
KW	Immunoglobulin V region.								
FT	DOMAIN 1 114								
FT	DISULFID 22 98								
FT	NON_TER 115 115								
SQ	SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;								
Query Match 52.6%; Score 349; DB 1; Length 115;									
Best Local Similarity 58.1%; Pred. No. 2.2e-26;									
Matches 72; Conservative 14; Mismatches 26; Indels 12; Gaps 2;									
QY	2	VTLDESGGLQTPGGALSLVCKASGFTFSSHGCMWVROTTPGKLEWVAGI--SNTGTYTY	59						
DB	2	VKLEESGGGLVQPGGSMKLSVCVSGFTFSNYNMWVYRQSPKEGLEWVAEIRLKSNNYATH	61						
QY	60	YAPAVKGRATISRONGQSTVRLQLNNLRADTGTYTCAGKGYACAGCGGDIDAWGHGTEV	119						
DB	62	YAESVKGRFTISRDDSKSSVLYOMNLRADETGIYCTTGTFAY-----WGQGLV	111						
QY	120	IVSS 123							
DB	112	TVSA 115							
RESULT 2									
ID	HV3K_HUMAN								
STANDARD;									
PRT;	126 AA.								

P01789 mus musculus
P01790 mus musculus
P01794 mus musculus
P01766 homo sapien
P01787 mus musculus
P01788 mus musculus
P01813 caiman croc
P01792 mus musculus
P01773 homo sapien
P19180 carassius a
P01786 mus musculus
P01791 mus musculus

34 310.5 46.8 122 1 HV20_MOUSE
35 310.5 46.8 122 1 HV21_MOUSE
36 309 46.6 123 1 HV25_MOUSE
37 308 46.5 120 1 HV3E_HUMAN
38 308 46.5 123 1 HV18_MOUSE
39 307 46.3 123 1 HV19_MOUSE
40 306 46.2 117 1 HV01_CAICR
41 304 45.9 123 1 HV23_MOUSE
42 302 45.6 119 1 HV3L_HUMAN
43 300 45.2 117 1 HV03_CARAU
44 300 45.2 117 1 HV17_MOUSE
45 300 45.2 123 1 HV22_MOUSE

AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RL immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GIHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 112 IG-LIKE.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;
Query Match 52.4%; Score 347.5; DB 1; Length 126;
Best Local Similarity 57.1%; Pred. No. 3.3e-26;
Matches 72; Conservative 17; Mismatches 32; Indels 5; Gaps 3;
QY 2 VTLDSEGGGLQTPGGALSVCRASTGFTFSHGMMWVQTPGKLEWVAGISNTGTYTYA 61

Db 2 VOLVESGGGVQPGSLRLSCSSSGFTFSSYAMVVRQAPGKLEWVAGISNTGTYTYA 61
QY 62 PAVKGRATISRDNGQSTVRLQLNLRADETGTYCAKGG--AYC--AGCGDDIDANGHGT 117
Db 62 DSVKGRFTISRDNSKNTFLQMDSLRPEDTGVYFCARDGSGHGFCSASCSP--DYWGQGT 120
QY 118 EVIVSS 123
Db 121 PVTVSS 126
RESULT 3
HV3C_HUMAN STANDARD; PRT; 117 AA.
ID P01764;
AC P01764; (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RL heavy chain variable region.";
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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CC -----
DR EMBL; J00236; AA53516.1; -.
DR EMBL; M35415; AA58735.1; -.
DR PIR; A02047; H3HU26.
DR PDB; 1HOU; 23-DEC-99.
DR Genes; HGNC:5545; IGHV6.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
Query Match 52.2%; Score 346; DB 1; Length 117;
Best Local Similarity 68.0%; Pred. No. 4.2e-26;
Matches 66; Conservative 10; Mismatches 21; Indels 0; Gaps 0;
QY 2 VTLDSEGGGLQTPGGALSVCRASTGFTFSHGMMWVQTPGKLEWVAGISNTGTYTYA 61
Db 21 VQLLESGGLVQPGSLRLSCASGFTFSSYAMVVRQAPGKLEWVAGISNTGTYTYG 80
QY 62 PAVKGRATISRDNGQSTVRLQLNLRADETGTYCAK 98
Db 81 DSVKGRFTISRDNSKNTFLQMDSLRPEDTGVYFCARDGSGHGFCSASCSP--DYWGQGT 117

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RESULT 4
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00522; AADI5290.1; -.
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 1
FT CHAIN 16
FT DOMAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98BDB3F7016 CRC64;

Query Match 52.0%; Score 344.5; DB 1; Length 136;
Best Local Similarity 59.0%; Pred. No. 6.8e-26;
Matches 72; Conservative 12; Mismatches 35; Indels 3; Gaps 1;

QY 2 VLTDSGGGLQTPGGALSVCASGFTFSHGMMWVRQTPGKGLEWAGISNTGYTYA 61
Db 18 VOLVESGGGLVQPGSGRKLSCASGFTFSFGHWRQAPKPLEWYVYSSGSLHYA 77
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGAYCAGCGGDIDAWGHGTEIV 121
Db 78 DTVKGRFTISRDNPKNTLQMTSLASEDTAMTYCARGNYPYA---MDVWGQGTSTV 134
QY 122 SS 123

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Db 135 SS 136

RESULT 5
HV35_MOUSE
ID HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
RT between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
CC REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02074; MMS576.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT NON_TER 1
FT DOMAIN <1 110 IG-LIKE.
FT NON_TER 111
FT NON_TER 111
SQ SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Query Match 51.7%; Score 342.5; DB 1; Length 111;
Best Local Similarity 58.8%; Pred. No. 8.6e-26;
Matches 70; Conservative 14; Mismatches 26; Indels 9; Gaps 2;

QY 6 ESGGLQTPGGLSVCASGFTFSHGMMWVRQTPGKGLEWAGIS-NTGYTYAPAV 64
Db 1 ESGGLVQPGSGMKLSCVAGFTFSNNWVRQSPKGLEWVAEIRLKSQYTHAESV 60
QY 65 KGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGAYCAGCGGDIDAWGHGTEIVSS 123
Db 61 KGRFTISRDDSKSSVYLQNNLRAEDTGTYYCTPCGV-----PDYWGQGTTLTVSS 111

RESULT 6
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01796;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

```

```
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; A93818; AVMSAB.
DR HSP; P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 13675 MW; 76658C121C598285 CRC64;

Query Match 51.6%; Score 342; DB 1; Length 113;
Best Local Similarity 58.2%; Pred. No. 9.7e-26;
Matches 71; Conservative 13; Mismatches 26; Indels 12; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSHGMMWVROTQPGKLEWVAGI--SNTGTYTY 59
DB 2 VKLEESGGGLVQPGGSKLSCVASGFTFSNYWNVVRSQPEKLEWVAIRLKSHNYATH 61
QY 60 YAPAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAKGGAYCAGCGGDIDAWHGTEV 119
DB 62 YAESVKGREFTISRDKSSVYLQMNLRADTGTYCTGFAY-----WGQGTLV 111
QY 120 IV 121
DB 112 TV 113

RESULT 7
HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W.; Putnam F.W.;
RT Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUAM.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
```

```
Query Match 51.4%; Score 340.5; DB 1; Length 122;
Best Local Similarity 57.1%; Pred. No. 1.5e-25;
Matches 72; Conservative 13; Mismatches 32; Indels 9; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSHGMMWVROTQPGKLEWVAGISNTGTYTYA 61
DB 2 VELVESGGGVZPGRSLRSLSCAASGFTFSNYAMHWVROPQPGKLEWVAISYBGBKYYA 61
QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAK-----GAYCAGCGGDIDAWHGHT 117
DB 62 BSVKGRFTISRDBSKBTLQMNLSRAETAVTYCARDRLYGBYRA-----FNYWGQGT 116
QY 118 EVIVS 123
DB 117 LVTVS 122

RESULT 8
HV28_MOUSE
ID HV28_MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M.; Rudikoff S.; Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSP; P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 51.3%; Score 340; DB 1; Length 113;
Best Local Similarity 58.2%; Pred. No. 1.5e-25;
Matches 71; Conservative 13; Mismatches 26; Indels 12; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSHGMMWVROTQPGKLEWVAGI--SNTGTYTY 59
DB 2 VKLEESGGGLVQPGGSKLSCVASGFTFSNYWNVVRSQPEKLEWVAIRLKSHNYATH 61
QY 60 YAPAVKGRATISRDNQSTVRLQNLNRAEDTCTYYCAKGGAYCAGCGGDIDAWHGTEV 119
DB 62 YAESVKGREFTISRDKSSVYLQMNLRADTGTYCTGFAY-----WGQGTLV 111
QY 120 IV 121
DB 112 PV 113

RESULT 9
HV33_MOUSE
ID HV33_MOUSE STANDARD; PRT; 115 AA.
```


QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTQPKGLEWVAGI--SNTGTITY 59
 Db 2 VKLEESGGGLVQPGGSMKLSVASGFTFSNVMWVROSPKGLEWVAEIRLKSHNYATH 61
 QY 60 YAPAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGAYCAGCGDIDAWGHGTEV 119
 Db 62 YAESVKGRTISRDSKSSVYLQMNLRADTAIYCYGTGFAY-----WGQGTLY 111
 QY 120 IV 121
 Db 112 TV 113

RESULT 12
 HV3B_HUMAN
 ID HV3B_HUMAN STANDARD; PRT; 114 AA.
 AC P01763;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 112 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match
 Best Local Similarity 50.6%; Score 335.5; DB 1; Length 114;
 Matches 66; Conservative 20; Mismatches 27; Indels 9; Gaps 1;
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTQPKGLEWVAGISNTGTITYA 61
 Db 2 VOLVDSGGGLVQPGGSMKLSVASGFTFSNVMWVROSPKGLEWVAEIRLKSHNYATH 61
 QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGAYCAGCGDIDAWGHGTEV 121
 Db 62 DSVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGAYCAGCGDIDAWGHGTEV 121
 QY 122 SS 123
 Db 113 SS 114

RESULT 13

HV29_MOUSE
 ID HV29_MOUSE STANDARD; PRT; 113 AA.
 AC P01798;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78158406; PubMed=417344;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Sequence variation among heavy chains from Inulin-binding myeloma
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; C93818; AVMS09.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >113 IG-LIKE.
 FT DISULFID 22 98
 FT NON_TER 113 113 BY SIMILARITY.
 SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;
 Query Match
 Best Local Similarity 50.5%; Score 335; DB 1; Length 113;
 Matches 69; Conservative 15; Mismatches 26; Indels 12; Gaps 2;
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTQPKGLEWVAGI--SNTGTITY 59
 Db 2 VKLEESGGGLVQPGGSMKLSVASGFTFSNVMWVROSPKGLEWVAEIRLKSHNYATH 61
 QY 60 YAPAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGAYCAGCGDIDAWGHGTEV 119
 Db 62 YAESVKGRTISRDSKSSVYLQMNLRADTAIYCYGTGFAY-----WGQGTLY 111
 QY 120 IV 121
 Db 112 TV 113

RESULT 14
 HV3H_HUMAN
 ID HV3H_HUMAN STANDARD; PRT; 122 AA.
 AC P01769;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
 RL Biochemistry 13:2482-2498(1974).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02052; M3HUGA.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 50.3%; Score 333.5; DB 1; Length 122;
Best Local Similarity 52.5%; Pred. No. 6.7e-25;
Matches 64; Conservative 19; Mismatches 38; Indels 1; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPCKGLEWVAGISNTGTYTYA 61
DB 2 VZLVZSGGAVZPGRSLRUSCAASGFSFYAMHWVRQAPGKGLZWLVSISYBGBZYIA 61
QY 62 YPAVKGRATISRDNQSQSTVRLQLNNLRAEDTGTYYCAKGGAYCAGCGGIDIDAWHGTEV 121
DB 62 ASVKGRTISRBBKTMYLEMNSLRANTAVYCARSGIALGSVAG-TDYWGZGLTYI 120
QY 122 SS 123
DB 121 SS 122

RESULT 15
ID HV31_MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (rel. 01, Created)
DT 01-OCT-1993 (rel. 27, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A92810; AVMS57.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 50.2%; Score 333; DB 1; Length 113;
Best Local Similarity 57.4%; Pred. No. 6.9e-25;
Matches 70; Conservative 13; Mismatches 27; Indels 12; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPCKGLEWVAGI--SNTGTYTY 59
DB 2 VKLEESGGGLVQPGGSMKLSVCVASGFTFSNYWNVWVRQSPKLEWVAEIRLKSHNYETH 61
QY 60 YPAVKGRATISRDNQSQSTVRLQLNNLRAEDTGTYYCAKGGAYCAGCGGIDIDAWHGTEV 119
DB 62 YAESVKGRTISRDDSKSSVYLQMNILRAEDTGIYYCTTGFAI-----WGQGTLV 111
QY 120 IV 121
DB 112 TV 113

Search completed: September 3, 2003, 12:10:16
Job time : 5.65885 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	373	56.3	113	4	Q9UL90	homo sapien
2	372	56.1	597	4	Q96BB9	homo sapien
3	368.5	55.6	147	4	Q9Y509	homo sapien
4	365	55.1	119	11	Q9Z0E7	homo sapien
5	364.5	55.0	471	4	Q8TC77	mus musculus
6	363.5	54.8	118	4	Q9UL91	homo sapien
7	363.5	54.8	613	4	Q8WUK1	homo sapien
8	363	54.8	116	4	Q9UL93	homo sapien
9	359	54.1	121	4	Q9UL71	homo sapien
10	357.5	53.9	487	11	Q99KA4	mus musculus
11	352.5	53.2	494	4	Q96K68	homo sapien
12	351.5	53.0	122	4	Q9UL84	homo sapien
13	349	52.6	479	11	Q91WP5	mus musculus
14	349	52.6	499	4	Q8N5K4	homo sapien
15	348.5	52.6	573	4	Q8WU38	homo sapien
16	341	51.4	480	11	Q91XE1	mus musculus

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Db 2 VOLVESGGVQVPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLWFAFIRYDGSNKYYA 61
QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCAGGAYCAGCGGIDAWHGTEVIV 121
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYCAK-----DLNHWGGTTLTV 111

122 SS 123
||
112 SS 113

RESULT 2
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL EMBL: BC015760; AAH15760.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
Query Match 56.1%; Score 372; DB 4; Length 597;
Best Local Similarity 62.1%; Pred. No. 1.5e-27;
Matches 77; Conservative 11; Mismatches 34; Indels 2; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSHGMMWVRQTPGKGLWVAGISNTGTYTYA 61
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
21 VOLVESGGVQVPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLWVSAISGGSTYYA 80

QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCAGGAYCAGCGGIDAWHGTEV 119
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
81 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYCAKDPRGYSASGNTYREDYWGOGTLV 140

120 IVSS 123
|||
141 TVSS 144

RESULT 3
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE WH3 protein (Fragment).
GN WH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
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RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
Query Match 55.8%; Score 368.5; DB 4; Length 147;
Best Local Similarity 60.0%; Pred. No. 6.2e-28;
Matches 75; Conservative 13; Mismatches 34; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSHGMMWVRQTPGKGLWVAGISNTGTYTYA 61
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
2 VHLVESGGVQVPGKSLRLSCAASGFTFSYGMWVRQAPGKGLDWALLSYDGSSTYYA 61

QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCAGGAYCAGCG---GDIDAWHGTE 118
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
62 GSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYCAKDNYSVGYAGIDYWGOGTL 121

119 VIYSS 123
|||
122 TVVSS 126

RESULT 4
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ackin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307937; AAL09421.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;
Query Match 55.1%; Score 365; DB 11; Length 119;
Best Local Similarity 59.8%; Pred. No. 1e-27;
Matches 73; Conservative 15; Mismatches 30; Indels 4; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSHGMMWVRQTPGKGLWVAGISNTGTYTYA 61
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
2 VOLVESGGDLVPGGSLKLSAASGFTFSYGMWVRQTPDKRLWVATISSGGSTYYP 61

QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCAGGAYCAGCGGIDAWHGTEV 121
Db :||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYCAKDNYSVGYAGIDYWGOGTLV 117
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		PRT;	121 AA.
Q9UL7I	PRELIMINARY;		
ID Q9UL71; AC			
DT 01-MAY-2000	(TREMBLrel. 13, Created)		
DT 01-WAY-2000	(TREMBLrel. 13, Last sequence update)		
DT 01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. OX NCBI_Taxid=9606;			
[1]			
RN SEQUENCE FROM N.A.			
RP MEDLINE=98277139; PubMed=9614934;			
RX Wu X., Liu B., Van der Meijne P.L., Kalis N.N., Berney S.M., RA Young D.C.;			
"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".			
RL Clin. Immunol. Immunopathol. 87:184-192(1998). DR EMBL; AF095043; AAD56279.1; -. DR HSSP; P01772; 2FB4.			

Query Match	53.9%	Score	357.5	DB 11;	Length	487;			
Best Local Similarity	58.9%;	Pred. No.	3e-26;						
Matches	73;	Conservative	15;	Mismatches	33;	Indels	3;	Gaps	2;
Qy	2	VTLDESGGGIQTGGGALS LVCCKASGTFSSHGMWVRQTPGKGLEWVAGISNTGTYYA	61						
Db	21	VQLVESGGGLVKPGSILKSAAASGTFSSYAMSVWRQTPKRLWEVATISDGSVYYP	80						
Qy	62	PAVKGRTISRDNCGSTVRLQNLNRAETGTYYCAK--GGAYCACGGGDIDAWGHGTEV	119						
Db	81	DNVKGRTISRDAKNLNLYLQMHLKSEDTAMTYCARDMGSPGYG-SRFDYWGOGTTI	139						
Qy	120	IIVS	123						
Db	140	TVSS	143						
RESULT	11								

DR	HSSP; P01772; 2FB4.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 1.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
FT	NON_TER 122 122
FT	NON_TER 1
SQ	SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;
Query Match 53.0%; Score 351.5; DB 4; Length 122;	
Best Local Similarity 57.0%; Pred. No. 2.1e-26;	
Matches 73; Conservative 12; Mismatches 30; Indels 13; Gaps 2;	
QY	2 VTLDESGGGLQTPTGGALSIVCKASGTFSSHGHMMWVROTPOKGLEWAGISNTGTYYA 61 : : : : :
Db	2 VOLVESGGGVQPGRSLRLESCAASRTFESNYGMHWVRQAPCKGLEWAAAINSDGNKFYA 61 : : : : :
QY	62 PAVKGRATISRDNOSTVRLQLNNLRAEDTGYTCACG-----CAYCAGCGGDIDAWCH 115 : : : : :
Db	62 DSVGRGRTIFRDNKNMMDLQNSLRADTAFFVYCAKDGRRLVGTY-----FDYWGQ 114 : : : : :
QY	116 GTEVIVSS 123
Db	115 GTLVTVSS 122
RESULT 13	
Q91WP5 PRELIMINARY; PRT; 479 AA.	
ID	Q91WP5 AC
AC	Q91WP5;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Hypothetical 51.6 kDa protein.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RC	SEQUENCE FROM N.A.
RP	TISSUE=Colon;
RA	Strausberg R.;
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC013656; AAH13656.1; -
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 4.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS00835; IG_LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; 2.
KW	Hypothetical protein.
SQ	SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
Query Match 52.6%; Score 349; DB 11; Length 479;	
Best Local Similarity 55.7%; Pred. NO. 1.9e-25;	
Matches 68; Conservative 17; Mismatches 29; Indels 8; Gaps 1;	
QY	2 VTLDESGGGLQTPTGGALSIVCKASGTFSSHGHMMWVROTPOKGLEWAGISNTGTYYA 61 : : : : :
Db	21 VOLVESGGGLVKPGCSLVKSCAASGLTFSNYAMSWVRQSPEKRLEWAAAINSGNGTYYS 80 : : : : :
QY	62 PAVKGRATISRDNOSTVRLQLNNLRAEDTGYTCACGAYCACGCCGGDIDAWHGHEVT 121 : : : : :
Db	81 DTMKGRRTISRDNASTLYLQNSSLRSDDTAFFVYCVRGYF-----DYWGACTATV 132 : : : : :
QY	122 SS 123
Db	133 SS 134

Q8WU38	PRELIMINARY;	PRT;	573 AA.
ID	Q8WU38		
AC	Q8WU38;		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
DE	OS Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Tonsil;		
RC	Strasbourg R.;		
RA	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; BC021276; AAH21276.1;		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003006; Ig-MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF000047; Ig; 4.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 2.		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: September 3, 2003, 12:00:29 ; Search time 35.9514 Seconds
(without alignments)
547.464 Million cell updates/sec

Title: US-10-083-424A-20

Perfect score: 650

Sequence: 1 AVTLDESGGLTPGALS.....RGSTGIDAWHGTEIVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	507.5	78.1	146	19 AAW60170	Chicken Mab heavy
2	499	76.8	145	19 AAW60171	Heavy chain variab
3	491.5	75.6	129	22 AAG78977	Chicken protein #1
4	491	75.5	147	19 AAW60173	Heavy chain variab
5	471	72.5	141	19 AAW60172	Heavy chain variab
6	469.5	72.2	269	21 AAV71010	Chicken phospholam
7	402	61.8	96	23 AAG60417	Selective targetin
8	392	60.3	124	22 AAE07018	Human heavy chain
9	389.5	59.9	384	22 AAM24101	Human EST encoded

10	388	59.7	132	23 ABG69154	Human monoclonal a
11	385	59.2	177	24 AB336939	Anti-CD40 monoclon
12	384	59.1	132	23 ABG69150	Human monoclonal a
13	383	58.9	252	23 ABP45508	Human BlyS binding
14	382	58.8	247	23 ABP44985	Human BlyS binding
15	381.5	58.7	115	21 AAB39519	Anti-IL12 antibody
16	381	58.6	131	22 AAG65566	Amino acid sequenc
17	380.5	58.5	121	23 ABG76929	Humanised antibody
18	380.5	58.5	159	22 AAU14226	Human novel protei
19	380	58.5	126	23 ABG69155	Human monoclonal a
20	379.5	58.4	119	23 AAE28151	Human consensus he
21	379	58.3	122	14 AAR30773	Consensus humanise
22	379	58.3	125	22 AAB62746	Human HIV-1 monocl
23	379	58.3	132	22 AAU00576	VH ligand-binding
24	379	58.3	132	22 AAU00581	Modified VH ligand
25	379	58.3	132	22 AAU00584	Modified VH ligand
26	379	58.3	132	23 ABG69149	Human monoclonal a
27	379	58.3	132	23 ABG69152	Human monoclonal a
28	379	58.3	140	18 AAM13524	Anti-melanoma anti
29	379	58.3	247	23 ABP45319	Human BlyS binding
30	378.5	58.2	117	22 AAE12061	Human anti-tissue
31	378.5	58.2	123	18 AAW08582	Human antibody C4.
32	378.5	58.2	248	23 ABP45865	Human BlyS binding
33	378.5	58.2	313	22 AAU14320	Human novel protei
34	378	58.2	239	23 ABP45911	Human BlyS binding
35	378	58.2	243	23 ABP45924	Human BlyS binding
36	378	58.2	252	23 ABP45190	Human BlyS binding
37	377.5	58.1	115	22 AAB69601	Huntingtin minimal
38	377.5	58.1	239	22 AAB69603	Huntingtin intrabo
39	377	58.0	128	22 AAE07014	Human heavy chain
40	377	58.0	245	20 AAY06717	Antibody 12B5 sing
41	377	58.0	249	23 ABP45094	Human BlyS binding
42	376.5	57.9	127	22 AAG93584	Human anti-Rh(D) c
43	376	57.8	122	20 AAW78432	Antibody heavy cha
44	376	57.8	122	23 ABB9975	Heavy chain variab
45	376	57.8	132	23 ABG69151	Human monoclonal a

ALIGNMENTS

RESULT 1
AAW60170
ID AAW60170 standard; Protein; 146 AA.
XX
AC AAW60170;
XX
DT 23-SEP-1998 (first entry)
XX
DE Chicken Mab heavy chain variable domain sequence.
XX
DE Chicken: monoclonal antibody; MAB; immortalisation; immunisation;
KW Cystic fibrosis transmembrane conductance regulator; cystic fibrosis;
KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
KW transforming growth factor beta; CFTR; TGF beta.
XX
OS Gallus sp.
XX
PN WO9822510-A2.
XX
XX 28-MAY-1998.
PD
PF 18-NOV-1997; 97WO-US21077.
XX
XX 18-NOV-1996; 96US-0751359.
PR
XX (ARCH-) ARCH DEV CORP.
PA (UABR-) UAB RES FOUND.
XX
XX Accavitti MAV, Michael NM, Thompson CB;
XX WPI; 1998-312421/27.
DR
XX

PT Production of new monoclonal antibodies - by immunising chickens and
 PT immortalising B cells, used for, e.g. diagnosis and passive
 PT treatment of disease

XX Example 2; Page 61; 97pp; English.

CC This represents the amino acid sequence of the heavy chain variable
 CC domain of a chicken monoclonal antibody (MAB). The invention provides a
 CC method of producing chicken MAB against a variety of antigens. The
 CC method comprises immunising a chicken with an antigen and isolating a
 CC immortalising B cells. From a selected antibody-producing B cell,
 CC nucleic acid containing antigen-binding exons of the light and heavy
 CC chain genes is prepared. The heavy and light chain nucleic acid are
 CC cloned separately in vectors that encode the constant and leader
 CC regions of the heavy and light chains. The vectors are transferred to
 CC host cells which are cultured and the MAB is isolated. Such antibodies
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator)
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and
 CC carbohydrates. The MAB can be raised against antigenic determinants that
 CC do not normally induce a response in mammals. The structure of the
 CC chicken immunoglobulin (Ig) gene is such that even after diversification
 CC by repeated gene conversions and maturation, the genomic DNA of the
 CC expressed locus will always have the same L-V (leader-variable) intron
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the
 CC antigen-binding domain of rearranged chicken genes are known with
 CC certainty, allowing specific amplification with a single set of primers.
 CC The method is particularly used to produce MAB against mammalian antigens
 CC with highly conserved epitopes. The MABs are used for separation,
 CC detection, quantification or removal of antigens, particularly for
 CC diagnosis, including in vivo imaging. They are useful as
 CC immunohistochemical reagents, and for passive treatment of diseases,
 CC such as cystic fibrosis.

XX Sequence 146 AA;

Query Match 78.1%; Score 507.5; DB 19; Length 146;
 Best Local Similarity 80.3%; Pred. No. 8e-38;
 Matches 102; Conservative 7; Mismatches 15; Indels 3; Gaps 1;
 QY 1 AVTLDSEGGGLQTPGGALSIVCKASGDFSSYMIWVROAPGKLEYVAGIRSDGSIY 60
 DB 20 AVTLDSEGGGLQTPGGALSIVCKASGTFSSYNGWVROAPGKLEYVAGIRSDGSIY 60
 QY 61 GAAVKGRATISRDNGOSTLRQLNNLRADDTGYTCYCAK---SSYGSWRGSGTDIDAWGHG 79
 DB 80 GSAVKGRATISRDNGOSTLRQLNNLRADDTGYTCYCAK---SSYGSWRGSGTDIDAWGHG 117
 QY 118 TEVIVSS 124
 DB 140 TEVIVSS 146

RESULT 2

AAW60171
 ID AAW60171 standard; Protein; 145 AA.

AC AAW60171;

XX 23-SEP-1998 (first entry)

DE Heavy chain variable domain sequence of anti-CFTR 4-9.

XX Chicken; monoclonal antibody; MAB; immortalisation; immunisation;
 KW cystic fibrosis transmembrane conductance regulator; immunisation;
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
 KW transforming growth factor beta; CFTR; TGF beta.

OS Gallus sp.

XX W09822510-A2.

PN 28-MAY-1998.

XX

XX

PF 18-NOV-1997; 97WO-US21077.

XX 18-NOV-1996; 96US-0751359.

XX (ARCH-) ARCH DEV CORP.

PA (UABR-) UAB RES FOUND.

XX Accavitti MAV, Michael NM, Thompson CB;

XX WPI; 1998-312421/27.

XX Production of new monoclonal antibodies - by immunising chickens and

PT immortalising B cells, used for, e.g. diagnosis and passive

PT treatment of disease

XX Example 2; Page 61; 97pp; English.

XX This represents the amino acid sequence of the heavy chain variable

CC domain of anti-CFTR 4-9. The invention provides a method for producing

CC chicken monoclonal antibodies (MAB) against a variety of antigens. The

CC method comprises immunising a chicken with an antigen and isolating and

CC immortalising B cells. From a selected antibody-producing B cell,

CC nucleic acid containing antigen-binding exons of the light and heavy

CC chain genes is prepared. The heavy and light chain nucleic acid are

CC cloned separately in vectors that encode the constant and leader

CC regions of the heavy and light chains. The vectors are transferred to

CC host cells which are cultured and the MAB is isolated. Such antibodies

CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),

CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and

CC carbohydrates. The MAB can be raised against antigenic determinants that

CC do not normally induce a response in mammals. The structure of the

CC chicken immunoglobulin (Ig) gene is such that even after diversification

CC by repeated gene conversions and maturation, the genomic DNA of the

CC expressed locus will always have the same L-V (leader-variable) intron

CC and J (junction)-3' flanking sequences. Thus the sequences flanking the

CC antigen-binding domain of rearranged chicken genes are known with

CC certainty, allowing specific amplification with a single set of primers.

CC The method is particularly used to produce MAB against mammalian antigens

CC with highly conserved epitopes. The MABs are used for separation,

CC detection, quantification or removal of antigens, particularly for

CC diagnosis, including in vivo imaging. They are useful as

CC immunohistochemical reagents, and for passive treatment of diseases,

CC such as cystic fibrosis.

XX Sequence 145 AA;

Query Match 76.8%; Score 499; DB 19; Length 145;

Best Local Similarity 82.9%; Pred. No. 4.6e-37;

Matches 107; Conservative 3; Mismatches 11; Indels 8; Gaps 4;

QY 1 AVTLDSEGGGLQTPGGALSIVCKASGDFSSYMIWVROAPGKLEYVAGIRSDGSIY 60

DB 20 AVTLDSEGGGLQTPGGALSIVCKASGTFSSYNGWVROAPGKLEYVAGIRSDGSIY 60

QY 61 GAAVKGRATISRDNGOSTLRQLNNLRADDTGYTCYCAKSSYGSWRGSGTGDIDAWGHG 78

DB 79 GAAVKGRATISRDNGOSTLRQLNNLRADDTGYTCYCAKSSYGSWRGSGTGDIDAWGHG 115

QY 116 HCTEVIVSS 124

DB 137 HCTEVIVSS 145

XX RESULT 3

AAW78977

ID AAG78977 standard; Protein; 129 AA.

XX AAG78977;

XX 16-JAN-2002 (first entry)

DE Chicken protein #1.
 XX Chicken; monoclonal antibody; scFv; single chain fragment of V region;
 KW prion disease; C lambda chain.
 KW Gallus domesticus.
 OS JP2001238676-A.
 PN 04-SEP-2001.
 PD 29-FEB-2000; 2000JP-0054875.
 XX 29-FEB-2000; 2000JP-0054875.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2001-610054/70.
 DR
 XX Preparing a chicken monoclonal antibody for diagnosing and treating
 PT various diseases such as prion disease, comprises using an expression
 PT vector
 XX Disclosure; Fig 10; 25pp; Japanese.
 XX The present invention relates to a method for preparing a chicken
 CC monoclonal antibody by gene recombination. The method involves using an
 CC expression vector prepared by introducing a gene encoding scFv (single
 CC chain fragment of V region) of a chicken monoclonal antibody to an
 CC expression vector in which a gene encoding chicken C lambda chain (L
 CC chain constant region) is introduced. The chicken monoclonal antibody
 CC can be used for diagnosing and treating various diseases such as prion
 CC disease. The present sequence was used to illustrate the present
 CC invention.
 XX
 XX Sequence 129 AA;
 SQ
 Query Match 75.6%; Score 491.5; DB 22; Length 129;
 Best Local Similarity 76.7%; Pred. No. 1.9e-36;
 Matches 99; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
 QY 1 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSGSSIIY 60
 DB 1 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSGSSIIY 60
 QY 61 GAAVKGRTATISRDNGQSTLRQLNLRRAEDTGTYYCAKSS----YGSWRGSGTDIDAWG 115
 DB 61 GSAVKGRTATISRDNGQSTLRQLNLRRAEDTGTYYCAKAGCXXXXXXXXTAGSIDAWG 120
 QY 116 HGTIVIVSS 124
 DB 121 HGTIVIVSS 129
 RESULT 4
 AAW60173
 ID AAW60173 standard; Protein; 147 AA.
 XX AAW60173;
 XX AAW60173;
 XX 23-SEP-1998 (first entry)
 DT Heavy chain variable domain sequence of antibody 8 of unknown specificity.
 DE Chicken; monoclonal antibody; MAb; immortalisation; immunisation;
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
 KW transforming growth factor beta; CFTR; TGF beta.
 XX Gallus sp.
 OS
 XX WO9822510-A2.
 PN
 XX

PD 28-MAY-1998.
 XX 18-NOV-1997; 97WO-US21077.
 XX 18-NOV-1996; 96US-0751359.
 XX (ARCH-) ARCH DEV CORP.
 PA (UABR-) UAB RES FOUND.
 XX Accavitti MAV, Michael NM, Thompson CB;
 XX WPI; 1998-312421/27.
 DR
 XX Production of new monoclonal antibodies - by immunising chickens and
 PT immortalising B cells, used for, e.g. diagnosis and passive
 PT treatment of disease
 XX
 PS Example 2; Page 61; 97pp; English.
 XX This represents the heavy chain variable domain of an antibody of unknown
 CC specificity used as a control. The invention provides a method for
 CC producing chicken monoclonal antibodies (MAb) against a variety of
 CC antigens. The method comprises immunising a chicken with an antigen and
 CC isolating and immortalising B cells. From a selected antibody-producing
 CC B cell, nucleic acid containing antigen-binding exons of the light and
 CC heavy chain genes is prepared. The heavy and light chain nucleic acid are
 CC cloned separately in vectors that encode the constant and leader
 CC regions of the heavy and light chains. The vectors are transferred to
 CC host cells which are cultured and the MAb is isolated. Such antibodies
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and
 CC carbohydrates. The MAb can be raised against antigenic determinants that
 CC do not normally induce a response in mammals. The structure of the
 CC chicken immunoglobulin (Ig) gene is such that even after diversification
 CC by repeated gene conversions and maturation, the genomic DNA of the
 CC expressed locus will always have the same L-V (leader-variable) intron
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the
 CC antigen-binding domain of rearranged chicken genes are known with
 CC certainty, allowing specific amplification with a single set of primers.
 CC The method is particularly used to produce MAb against mammalian antigens
 CC with highly conserved epitopes. The MAbs are used for separation,
 CC detection, quantification or removal of antigens, particularly for
 CC diagnosis, including in vivo imaging. They are useful as
 CC immunohistochemical reagents, and for passive treatment of diseases,
 CC such as cystic fibrosis.
 XX
 XX Sequence 147 AA;
 SQ
 Query Match 75.5%; Score 491; DB 19; Length 147;
 Best Local Similarity 78.1%; Pred. No. 2.4e-36;
 Matches 100; Conservative 5; Mismatches 19; Indels 4; Gaps 1;
 QY 1 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSGSSIIY 60
 DB 20 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSGSSIIY 79
 QY 61 GAAVKGRTATISRDNGQSTLRQLNLRRAEDTGTYYCAKSSYGSWRGS----TGDIDAWG 116
 DB 80 APAVKGRTATISRDNGQSTLRQLNLRRAEDTGTYYCAKAGSGCSDATAGSIDAWG 139
 QY 117 GTEIVIVSS 124
 DB 140 GTEIVIVSS 147
 RESULT 5
 AAW60172
 ID AAW60172 standard; Protein; 141 AA.
 XX AAW60172;
 XX AAW60172;
 XX 23-SEP-1998 (first entry)
 DT

XX DE Heavy chain variable domain sequence of anti-CFTR 15-16.
 XX KW Chicken; monoclonal antibody; MAB; immortalisation; immunisation;
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
 KW transforming growth factor beta; CFTR; TGF beta.
 OS Gallus sp.
 XX FH Key Location/Qualifiers
 FT Misc-difference 129 /note= "unknown"
 FT XX
 PN WO9822510-A2.
 XX PD 28-MAY-1998.
 XX PF 18-NOV-1997; 97WO-US21077.
 XX PR 18-NOV-1996; 96US-0751359.
 XX PA (ARCH-) ARCH DEV CORP.
 XX PA (UABR-) UAB RES FOUND.
 XX PI Accavitti MAV, Michael NM, Thompson CB;
 XX DR WPI; 1998-312421/27.
 XX PT Production of new monoclonal antibodies - by immunising chickens and
 PT immortalising B cells, used for, e.g. diagnosis and passive
 PT treatment of disease
 XX PS Example 2; Page 61; 97pp; English.
 XX CC This represents the amino acid sequence of the heavy chain variable
 CC domain of anti-CFTR 15-16. The invention provides a method for producing
 CC chicken monoclonal antibodies (MAB) against a variety of antigens. The
 CC method comprises immunising a chicken with an antigen and isolating and
 CC immortalising B cells. From a selected antibody-producing B cell,
 CC nucleic acid containing antigen-binding exons of the light and heavy
 CC chain genes is prepared. The heavy and light chain nucleic acid are
 CC cloned separately in vectors that encode the constant and leader
 CC regions of the heavy and light chains. The vectors are transferred to
 CC host cells which are cultured and the MAB is isolated. Such antibodies
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and
 CC carbohydrates. The MAB can be raised against antigenic determinants that
 CC do not normally induce a response in mammals. The structure of the
 CC chicken immunoglobulin (Ig) gene is such that even after diversification
 CC by repeated gene conversions and maturation, the genomic DNA of the
 CC expressed locus will always have the same L-V (leader-variable) intron
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the
 CC antigen-binding domain of rearranged chicken genes are known with
 CC certainty, allowing specific amplification with a single set of primers.
 CC The method is particularly used to produce MAB against mammalian antigens
 CC with highly conserved epitopes. The MABs are used for separation,
 CC detection, quantification or removal of antigens, particularly for
 CC diagnosis, including in vivo imaging. They are useful as
 CC immunohistochemical reagents, and for passive treatment of diseases,
 CC such as cystic fibrosis.
 XX SQ Sequence 141 AA;

Query Match 72.5%; Score 471; DB 19; Length 141;
 Best Local Similarity 79.2%; Pred. No. 1.4e-34;
 Matches 99; Conservative 2; Mismatches 20; Indels 4; Gaps 2;

QY 1 AVTLDESGGGLQTPGGGLSLVCKASGDFSSYDMWVRQAPGKLEYVAGIRSDGSIY 60
 Db 20 AVTLDESGGGLQTPGGGLSLVCKASGFTFSSNGWVRQAPGKLEYVAGISSGKYTG 79

QY 61 GAAVKGRTATSRDNGQSTLRQLNLRADTGTYYCAKSSYSGWRSRGTDID-ANGHGTG 119
 Db 80 GSAVKGRTATSRDNGQSTVRQLNLRADTATYYCAK---GGRSGFTCVISXTWGHGTG 136
 QY 120 VIVSS 124
 Db 137 VIVSS 141

RESULT 6

AAY71010
 ID AAY71010 standard; Protein; 269 AA.
 XX AAY71010;

XX 29-AUG-2000 (first entry)
 XX Chicken phospholamban (PLB) antibody, contractilin.

DE Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiomyocyte; transport peptide; penetratin; cargo peptide; chicken;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW cardiant; treatment; heart failure; myocardial dysfunction.

OS Gallus domesticus.

XX WO2000025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US25692.

XX 02-NOV-1998; 98US-0106718.

XX 27-JUL-1999; 99US-0145883.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase

XX Disclosure; Page 50-51; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is that of contractilin protein, a
 CC chicken antibody peptide with hyperactive regions. This is used to raise
 CC polyclonal PLB antibody, by immunising a chicken repeatedly with the
 CC human PLB peptide from the cytoplasmic domain (residues 3-19).

XX Sequence 269 AA;

Query Match 72.2%; Score 469.5; DB 21; Length 269;
 Best Local Similarity 75.2%; Pred. No. 4e-34;
 Matches 94; Conservative 9; Mismatches 19; Indels 3; Gaps 2;

QY 2 VTLDSEGGGLQTPGGGLSLVCKASGDFSSYDMWVRQAPGKLEYVAGIRSDGSIY 61
 Db 129 VTLDSEGGGLQTPGGGLSLVCKASGFTFSSRFHMMWVRQAPGKLEWVAGIDGGSTLYG 188

CC 82a-N, 93-A or 108-Q, in comparison to the parent human monoclonal
 CC antibody A6 heavy chain domain. The library (e.g. a combinatorial
 CC library for phage display) may comprise at least the framework region of
 CC A6 VH including the CDR region containing the target amino acids above.
 CC The libraries are useful in expressing a series of potential heavy chain
 CC binding domains for panning against the target ligand. The amino acid
 CC residues 6, 23, 82a, 93, and 108, particularly when combined, are
 CC useful in augmenting the solubility properties of a parental VH ligand
 CC binding fragment, preferably one like A6, which has useful solubility
 CC properties in producing a library of dAb variants for panning against a
 CC target ligand. The present sequence represents the human monoclonal
 CC antibody BT33/A6 (or just A6) heavy chain variable domain variant
 CC protein (either a created mutant or a representative of a combinatorial
 CC library of mutants).

SQ Sequence 132 AA;
 Query Match 59.7%; Score 388; DB 23; Length 132;
 Best Local Similarity 59.5%; Pred. No. 3.4e-27;
 Matches 78; Conservative 12; Mismatches 33; Indels 8; Gaps 1;
 QY 2 VTLDSEGGGLQTPGGALSILVCKASGDFSSYDMIVWROAPKGLGYVAGIRSDGSSIIYG 61
 Db 2 VQLQASGGGLVOPGGSLRUSCAASGFTFSYAMHWVROAPKGLGYVSAISNGGSTYYA 61
 QY 62 AAVKGRATISRNGQSTLRQLNLRRAEDTGYTCYAK-----SSYGSWRGSGTDIDA 113
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYCAKDLKVEYDSSGYNNNNNFDI 121
 QY 114 WGHGTEVIVSS 124
 Db 122 WGGTQTVVSS 132

RESULT 11
 ABJ36939
 ID ABJ36939 standard; Protein; 177 AA.
 AC ABJ36939;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE Anti-CD40 monoclonal antibody related protein SEQ ID No 64.
 XX
 KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
 KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
 KW immunosuppressor; anti-tumour agent; immunosuppressant; allergy;
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.
 OS Unidentified.
 OS
 XX WO200288186-A1.
 PN
 XX
 PD 07-NOV-2002.
 XX
 PF 26-APR-2002; 2002WO-JP04292.
 XX
 PR 27-APR-2001; 2001WO-US13672.
 PR 11-MAY-2001; 2001JP-0142482.
 PR 05-OCT-2001; 2001JP-0310535.
 PR 26-OCT-2001; 2001US-0040244.
 XX
 PA (KIRI) KIRIN BEER KK.
 XX
 PI Miyayama T, Yoshida H, Force WR, Chen X, Takahashi N;
 XX
 DR WPI; 2003-120463/11.
 DR N-PSDB; ABT31881.
 XX
 PT Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
 PT or functional fragment, is useful in the treatment of e.g. autoimmune
 PT diseases or cancer

XX Claim 15; Page 59; 94pp; Japanese.
 PS
 CC The invention relates to an antibody to human CD40, or its functional
 CC fragment, has at least one of the following properties: acting on
 CC dendritic cells to produce IL-12 in the presence of LPS
 CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
 CC cells to activate maturity of the dendritic cells with high G28-5
 CC antibody; and activating CD95 expression with high G28-5 antibody against
 CC B cell line. Such antibodies or functional fragments can be used as
 CC immunosuppressants, anti-tumour agents, immunosuppressants, and as remedies
 CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors
 CC syndrome. This sequence represents a protein relating to the anti-CD40
 CC monoclonal antibody of the invention.

SQ Sequence 177 AA;
 Query Match 59.2%; Score 385; DB 24; Length 177;
 Best Local Similarity 64.8%; Pred. No. 8.8e-27;
 Matches 81; Conservative 8; Mismatches 32; Indels 4; Gaps 2;
 QY 2 VTLDSEGGGLQTPGGALSILVCKASGDFSSYDMIVWROAPKGLGYVAGIRSDGSSIIYG 61
 Db 21 VQLLESGGLVOPGGSLRUSCAASGFTFSYAMSWVROAPKGLWVSAISGSGSTYYA 80
 QY 62 AAVKGRATISRNGQSTLRQLNLRRAEDTGYTCYAKSS--YGSWRGSGTDIDAWHGTE 119
 Db 81 DSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYCAKDGYYGS--GSYGYFDWVGOTL 138
 QY 120 VIVSS 124
 Db 139 VTVSS 143

RESULT 12
 ABG69150
 ID ABG69150 standard; Protein; 132 AA.
 XX
 AC ABG69150;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human monoclonal antibody BT33/A6 VH region variant A6VH-L1.
 XX
 KW Monoclonal antibody; BT33/A6; phage display; panning; framework region;
 KW Heavy chain variable region; CDR; complementarity determining region;
 KW combinatorial library; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200251870-A2.
 PN
 XX
 PD 04-JUL-2002.
 XX
 PF 21-DEC-2001; 2001WO-CA01845.
 XX
 PR 22-DEC-2000; 2000US-258031P.
 XX
 PA (GRAD/) GRAD C.
 PA (ENTW/) ENTWISTLE J.
 PA (TANH/) TANHA J.
 PA (NARA/) NARANG S.
 PA (DANM/) DAN M.
 PA (MACK/) MACKENZIE C R.
 XX
 PI Entwistle J, Tanha J, Narang S, Dan M, Mackenzie CR;
 XX
 DR WPI; 2002-575370/61.
 DR N-PSDB; ABK98579.
 XX
 PT New libraries comprising a repertoire of nucleic acid sequences
 PT encoding a polypeptide with a VH with CDR for expressing immunoglobulin

PT heavy chain binding domains for panning against the target ligand -
 XX Claim 12; Fig 2; 98pp; English.
 XX The invention relates to a library comprising a repertoire of nucleic
 CC acid sequences each encoding a polypeptide with a variable heavy (VH)
 CC domain with a Complementarity Determining Region (CDR) differing at
 CC least in CDR and comprising at least one of the amino acids 6-A, 23-A,
 CC 82a-N, 93-A or 108-Q, in comparison to the parent human monoclonal
 CC antibody A6 heavy chain domain. The library (e.g. a combinatorial
 CC library for phage display) may comprise at least the framework region of
 CC A6 VH including the CDR region containing the target amino acids above.
 CC The libraries are useful in expressing a series of potential heavy chain
 CC binding domains for panning against the target ligand. The amino acid
 CC residues 6, 23, 82a, 93, and 108, particularly when combined, are
 CC useful in augmenting the solubility properties of a parental VH ligand
 CC binding fragment, preferably one like A6, which has useful solubility
 CC properties in producing a library of dAb variants for panning against a
 CC target ligand. The present sequence represents the human monoclonal
 CC antibody B13/A6 (or just A6) heavy chain variable domain variant
 CC protein (either a created mutant or a representative of a combinatorial
 CC library of mutants).
 XX Sequence 132 AA;

Query Match 59.1%; Score 384; DB 23; Length 132;
 Best Local Similarity 60.3%; Pred. No. 7.8e-27;
 Matches 79; Conservative 10; Mismatches 34; Indels 8; Gaps 1;
 QY 2 VTLDSEGGGLQTPGGLSLVCKASGDFSSYDMWVRQAPGKLEYVAGIRSDGSSIIYG 61
 Db 2 VQLQASGGGLVQPGSLRLSCAASGFTFSYAMHWVRQAPGKLEYVSAISSNGSTYYA 61
 QY 62 AAVKGRATISRDNGQSTLRQLNNLRAEDTGTYYCAK-----SSYGSWRGSGTGDDA 113
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKRLKVEYDSSGVYVSRFGAFDI 121
 QY 114 WGHGTEIVYS 124
 Db 122 WGQGTQTVSS 132

RESULT 13
 ABP45508
 ID ABP45508 standard; Protein; 252 AA.
 AC ABP45508;
 XX 19-AUG-2002 (first entry)
 DE Human BlyS binding scFv SEQ ID 1519.
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX WO200202641-A1.
 PN 10-JAN-2002.
 PD 10-JAN-2002.
 XX 15-JUN-2001; 2001WO-US19110.
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX Claim 1; Page 2215-2216; 3148pp; English.
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX Sequence 252 AA;

Query Match 58.9%; Score 383; DB 23; Length 252;
 Best Local Similarity 63.4%; Pred. No. 2e-26;
 Matches 78; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
 QY 2 VTLDSEGGGLQTPGGLSLVCKASGDFSSYDMWVRQAPGKLEYVAGIRSDGSSIIYG 61
 Db 2 VQLQESGGVGVQPSRLSLSCAASGFTFSYGMHWVRQAPGKLEYVAVLSYDGSNKYYA 61
 QY 62 AAVKGRATISRDNGQSTLRQLNNLRAEDTGTYYCAKSSYGSWRGSGTGDDA HGHGTEVI 121
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKROYDILTYGGFDYWGQGTMTV 121
 QY 122 VSS 124
 Db 122 VSS 124

RESULT 14
 ABP44985
 ID ABP44985 standard; Protein; 247 AA.
 XX ABP44985;
 AC ABP44985;
 XX 19-AUG-2002 (first entry)
 DE Human BlyS binding scFv SEQ ID 996.
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX WO200202641-A1.
 PN 10-JAN-2002.
 PD 10-JAN-2002.
 XX 15-JUN-2001; 2001WO-US19110.
 PR

XX	
PR	16-JUN-2000; 2000US-212210P.
PR	17-OCT-2000; 2000US-240816P.
PR	16-MAR-2001; 2001US-276248P.
PR	21-MAR-2001; 2001US-277379P.
PR	25-MAY-2001; 2001US-293499P.
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	WPI; 2002-1114799/15.
DR	Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT	the diagnosis and treatment of cancers and immune disorders -
XX	Claim 1; Page 1590-1591; 3148pp; English.
PS	This invention describes novel antibodies that immunospecifically bind to
XX	B Lymphocyte stimulator (BLYS) polypeptides. BLYS is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	Inhibit the expression and activity of BLYS. The antibodies bind to Blys
CC	and so may be used to detect and quantitate the presence of BLYS in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of BLYS. They may also be
CC	administered to treat diseases associated with aberrant BLYS expression
CC	and activity such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method
CC	of the invention.
XX	
XX	Sequence 247 AA;
SQ	
	Query Match 58.8%; Score 382; DB 23; Length 247;
	Best Local Similarity 61.8%; Pred. No. 2.4e-26;
	Matches 76; Conservative 11; Mismatches 36; Indels 0; Gaps 0;
OY	2 VTLDSEGGGLQTFCGALSIVCKASGFDFSYDMMIWRQAPKGLEUYAGIRSDGSSYYIG 61 : : 2 VTLKESGGGVYPGRSLRLSCAASGETFFSSYGHWVVRQAPKGLEWVSALISGSSTTYIA 61
Dd	
OY	62 AAVKGRATISRDNQGQSTRLOLNLRADTGTYICAKSSYSGWSRGTDIDAWHGRTVI 121 : : : 62 DSVKGRFTISRDNKSNTLYLQMNSLRADTAHYCARSGVDILTGYLYGHMDVWGQGTNVT 121
Dd	
OY	122 VSS 124
Dd	122 VSS 124
	RESULT 15
AAB39519	ID IAB39519 standard; Protein; 115 AA.
XX	AAB39519;
AC	
XX	
DT	05-FEB-2001 (first entry)
XX	
DE	Anti-IL12 antibody H chain variable region amino acid sequence SEQ ID 35.
XX	
KW	Human; neutralising antibody; interleukin-12; IL-12; antinflammatory;
KW	complementarity determining region; CDR; antirheumatic; antiarthritic;
KW	antisclerotic; neuroprotective; antipsoriatic; anticlastmatic; cardiant;
KW	anti-parasitic; antibacterial; immunosuppressive; Crohn's disease;
KW	multiple sclerosis; rheumatoid arthritis.
OS	Homo sapiens.
XS	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:00:29 ; Search time 31.3125 Seconds
(without alignments)
547.464 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 A LQPSVSVANPGTVKTC.....GSFSSVYVILGAGTTLVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	459.5	81.6	269	AAV71010	Chicken phospholamban
2	449.5	79.8	126	AAW60167	Light chain variab
3	427	75.8	105	AAG78978	Chicken protein #2
4	426.5	75.8	126	AAW60166	Chicken Mab light
5	426	75.7	125	AAW60168	Light chain variab
6	423.5	75.2	124	AAW60169	Light chain variab
7	319.5	56.7	212	ABR01489	Human anti-TIMP-1
8	318.5	56.6	108	ABBS7560	HLA-DR-specific pr
9	318.5	56.6	212	ABR01497	Human anti-TIMP-1

10	318	56.5	111	18	AAW13528	Anti-melanoma ligh
11	318	56.5	249	23	ABP45301	Human BlyS binding
12	316.5	56.2	108	23	AAO18431	Anti-GD2 antibody
13	315.5	56.0	245	22	ABAB67622	Human leukocyte an
14	315	56.0	251	23	ABP45845	Human BlyS binding
15	315	56.0	251	23	ABP45829	Human BlyS binding
16	314.5	55.9	245	22	ABAB67619	Human leukocyte an
17	312	55.4	215	24	ABR01491	Human anti-TIMP-1
18	312	55.4	255	23	ABP45145	Human BlyS binding
19	311.5	55.3	245	22	ABAB67620	Human leukocyte an
20	311	55.2	211	24	ABR01471	Human anti-TIMP-1
21	311	55.2	211	24	ABR01495	Human anti-TIMP-1
22	310.5	55.2	245	22	ABAB67617	Human leukocyte an
23	310	55.1	258	23	ABP45249	Human BlyS binding
24	309.5	55.0	245	22	ABAB67618	Human leukocyte an
25	309	54.9	108	17	AAH88719	Human antibody lam
26	309	54.9	123	24	AAO19680	P aeruginosa MEP a
27	309	54.9	211	24	ABR01472	Human anti-TIMP-1
28	308.5	54.8	245	22	ABAB67621	Human leukocyte an
29	308	54.7	109	23	AAU83808	MS-GPC-10 light ch
30	308	54.7	109	23	ABBS7568	HLA-DR-specific pr
31	308	54.7	111	23	AAO18430	Anti-GD2 antibody
32	308	54.7	245	24	ABP60521	APRIL binding scFv
33	308	54.7	248	23	ABP44850	Human BlyS binding
34	308	54.7	258	23	ABP45018	Human BlyS binding
35	307.5	54.6	110	23	AAO18434	Anti-GD2 antibody
36	307.5	54.6	245	22	ABAB67623	Human leukocyte an
37	307	54.5	111	21	AAH82529	Carcinoembryonic a
38	307	54.5	215	24	ABR01480	Human anti-TIMP-1
39	306.5	54.4	214	24	ABR01470	Human anti-TIMP-1
40	306.5	54.4	245	23	ABP45853	Human BlyS binding
41	306.5	54.4	252	23	ABP45538	Human BlyS binding
42	306.5	54.4	252	23	ABP45981	Human BlyS binding
43	306	54.4	215	24	ABR01500	Human anti-TIMP-1
44	306	54.4	246	23	ABP46066	Human BlyS binding
45	306	54.4	253	23	ABP45848	Human BlyS binding

ALIGNMENTS

RESULT 1
AAV71010
ID AAV71010 standard; Protein; 269 AA.
XX
AC AAV71010;
XX
DT 29-AUG-2000 (first entry)
XX
DE Chicken phospholamban (PLB) antibody, contractilin.
XX
DE Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiomyocyte; transport peptide; penetratin; cargo peptide; chicken;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW cardiant; treatment; heart failure; myocardial dysfunction.
XX
OS Gallus domesticus.
XX
PN WO200025804-A2.
XX
PD 11-MAY-2000.
XX
PF 02-NOV-1999; 99WO-US25692.
XX
PR 02-NOV-1998; 98US-0106718.
PR 27-JUL-1999; 99US-0145883.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
PI Scott C, Wang Y, Silverman GJ;
XX
DR WPI; 2000-365393/31.

KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer..
 KW Homo sapiens.
 OS WO2000286085-A2.
 PN 31-OCT-2002.
 PD 24-APR-2002; 2002WO-US12801.
 PF 24-APR-2001; 2001US-285683P.
 PR (FARB) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 XX Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;
 XX WPI; 2003-129114/12.
 DR N-PSDB; ABZ74846.
 XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1)
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 PT hypertrophy or lung cancer -
 XX Claim 21; Page 138; 228pp; English.
 PS The invention relates to a novel purified preparation of a human
 XX antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)
 CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01450-ABR01501 represent the light
 CC chain regions of a human anti-TIMP-1 antibody of the invention.
 XX SQ Sequence 212 AA;
 Query Match 56.7%; Score 319.5; DB 24; Length 212;
 Best Local Similarity 60.7%; Pred. No. 7.1e-19;
 Matches 65; Conservative 10; Mismatches 29; Indels 3; Gaps 2;
 Qy 2 LTQPSVSNPGETVKITCSGGSYAGSYGYGWYQKAPASAPVTVIYDNTNRPSNIPSR 61
 Db 4 LTQPPSVVAPGQTARISCSGDA--LGDKYASWYQK-PGQAPVLVIYDDSDRPSGIPER 60
 Qy 62 FSGSLSGSTNTITRGVQVEDEAVYVCGSPDSYVGLGAGTTTLV 108
 Db 61 FSGNSGNTATLTISGTAQDEADYVCSYDLRYSHVFGGKTLTV 107
 RESULT 8
 ABB57560
 ID ABB57560 standard; Peptide; 108 AA.
 XX ABB57560;
 AC ABB57560;
 XX 18-MAR-2002 (first entry)
 DT HLA-DR-specific protein MS-GPC5 VL sequence.
 DE Immunomodulatory human MHC class II antigen-binding protein; HLA;
 KW human leukocyte antigen; immune system; immunosuppression; antibody;
 KW major histocompatibility complex; antirheumatic; antiarthritic;

KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
 KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;
 KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
 KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
 KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
 KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
 KW transplant rejection; graft versus host disease; pemphigus vulgaris;
 KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
 KW irritable bowel disease; Sjogren's syndrome.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200187338-A1.
 PN 22-NOV-2001.
 PD 14-MAY-2001; 2001WO-US15626.
 XX 12-MAY-2000; 2000EP-0110063.
 PR 06-OCT-2000; 2000US-238762P.
 XX (GPCB-) GPC BIOTECH AG.
 PA (MORP-) MORPHOSYS AG.
 XX Nagy Z, Tesar M, Thomassen-Wolf E;
 PI WPI; 2002-075289/10.
 DR Composition for suppressing immune response, treating diseases of
 XX immune system, has polypeptide comprising antibody-based
 PT antigen-binding domain of human composition, which binds antigen
 PT expressed on a cell surface -
 XX Example; Fig 15; 139pp; English.
 PS The present invention describes a composition (I), comprising a
 XX polypeptide comprising an antibody-based antigen-binding domain of human
 CC composition with binding specificity for an antigen expressed on the
 CC surface of a cell, where treating cells expressing the antigen with the
 CC polypeptides leads to suppression of an immune response, and the IC50 for
 CC the suppression of immune response is 1 microm or less. (I) has
 CC antineumatic, antiarthritic, neuroprotective, antiinflammatory,
 CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
 CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
 CC can be used as a suppressor of immune response. (I) is useful for
 CC suppressing activation or proliferation of a cell of the immune system,
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
 CC immune system with another cell, immunosuppressing a patient and for
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR
 CC on the surface of the cell, where neither cytotoxic entities nor
 CC immunological mechanisms are needed to cause or lead to the killing.
 CC (I) optionally linked to cytotoxic or immunogenic agent) is useful for
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 CC the exemplification of the present invention.
 XX SQ Sequence 108 AA;
 Query Match 56.6%; Score 318.5; DB 23; Length 108;
 Best Local Similarity 59.8%; Pred. No. 4.3e-19;
 Matches 64; Conservative 12; Mismatches 28; Indels 3; Gaps 2;
 Qy 2 LTQPSVSNPGETVKITCSGGSYAGSYGYGWYQKAPASAPVTVIYDNTNRPSNIPSR 61
 Db 4 LTQPPSVVAPGQTARISCSGDA--LGDKYASWYQK-PGQAPVLVIYDDSDRPSGIPER 60

QY 62 FSGSLSGSTNLTITGVQVEADAVYCGSFSSVYVILGAGTTLTVL 108
 DB 61 FSGNSGNATLTISGTQAEADAYCQSDVDNISVFGGKTLTVL 107

RESULT 9
 ID ABR01497 standard; Protein; 212 AA.
 AC ABR01497;
 XX
 DT 16-APR-2003 (first entry)
 DE Human anti-TIMP-1 antibody light chain #38.
 XX
 KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
 KW matrix metalloproteinase; MMP; variable heavy chain; VHCADR3; hepatotropic;
 KW variable light chain; cytotatic; nephrotropic; cardiant; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200286085-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 24-APR-2002; 2002WO-US12801.
 XX
 XX 24-APR-2001; 2001US-285683P.
 XX
 PA (FARB) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;
 DR WPI; 2003-129114/12.
 DR N-PSDB; ABZ74854.
 XX
 XX New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 PT hypertrophy or lung cancer.
 XX
 PS Claim 21; Page 143-144; 228pp; English.
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01460-ABR01501 represent the light
 CC chain regions of a human anti-TIMP-1 antibody of the invention.
 XX
 XX Sequence 212 AA;

Query Match
 Best Local Similarity 56.6%; Score 318.5; DB 24; Length 212;
 Matches 65; Conservative 11; Mismatches 28; Indels 3; Gaps 2;

QY 2 LTPQSVSANGETVKITCSGGSYAGSYVYQKAPASAPVTVVINDNRPNSIPSR 61
 DB 4 LIQPFVSVPQQTARISCSGDA--LGDKYASWYQK-PGQAPVLVIYDSDRPSGIPR 60

QY 62 FSGSLSGSTNLTITGVQVEADAVYCGSFSSVYVILGAGTTLTVL 108
 DB 61 FSGNSGNATLTISGTQAEADAYCQSDVDNISVFGGKTLTVL 107

RESULT 10
 ID ABR013528 standard; protein; 111 AA.
 XX
 AC ABR013528;
 XX
 DT 28-OCT-1997 (first entry)
 DE Anti-melanoma light chain antibody clone V373.
 XX
 KW Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
 KW cancer; tumourigenesis; anticancer vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region Location/Qualifiers
 FT 23..35
 FT /label= CDR1
 FT 51..57
 FT /label= CDR2
 FT 90..100
 FT /label= CDR3
 XX
 PN WO9702479-A2.
 XX
 XX 23-JAN-1997.
 XX
 XX 28-JUN-1996; 96WO-IB01032.
 XX
 XX 30-JUN-1995; 95US-0497647.
 XX
 XX (UYUA) UNIV YALE.
 XX
 XX Cai X, Garen A;
 XX
 XX WPI; 1997-109061/10.
 XX
 PT Prodn. of human monoclonal anti-tumour antibodies - by screening a
 PT fusion phase library produced using peripheral blood lymphocytes
 PT from a cancer patient
 XX
 PS Claim 19; Page 65; 82pp; English.
 CC A process for isolating and synthesising human monoclonal anti-tumour
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion phase library from the peripheral blood lymphocytes
 CC (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in
 CC the phase library in a binding assay with cultured tumour cells of the
 CC same type as the patient's tumour; (c) removing extraneous antibodies by
 CC absorption against normal human cells; (d) cloning the phase selected in
 CC step (b) and (c); (e) assaying the specificity of the cloned phase by
 CC incubating the phase with at least two types of cultured normal cells;
 CC and (f) further testing the specificity of cloned phase that do not bind
 CC to either cell line of cultured normal cells in further binding assays
 CC to cultured tumour cells derived from more than one other tumour that is
 CC not the patient's tumour. The present sequence represents a human light
 CC chain antibody, from an scfv antibody fusion phase library, produced by
 CC a method as described above. The antibodies produced can be used for
 CC diagnostic and therapeutic applications and for isolating tumour
 CC antigens for studying tumourigenesis or for use as anti-cancer vaccines.
 CC The human antibodies have low immunogenicity in humans compared to
 CC murine monoclonal antibodies (MABs). Since the antibodies are isolated
 CC from fusion phase libraries, their affinity and specificity for a
 CC tumour cell line can be improved by genetic manipulations.
 XX
 XX Sequence 111 AA;

Query Match	56.5%;	Score 318;	DB 18;	Length 111;
Best Local Similarity	59.6%;	Pred. No. 4.9e-19;		
Matches	65;	Conservative	12;	Mismatches 30; Indels 2; Gaps 2;
QY	1	ALTPQSSVSANPGETVKITCSGGGSYAGSYGYGYYOOKAPASAPVTVIYDNTNRPSPNIPS	60	
DB	3	ALTPQPSVSANPQKQVTITCSGSSSNTGNVYSWY-ORLPGTAPKLIYENNRKPSGIPD	61	
QY	61	RFGSSLSGSSNTTITGVOVEDEAVYCYGGSFDSYVG-ILGAGTTTLVL	108	
DB	62	RFGSSSGTSATLAIITGLQADEAGYCYQSDYVSGVFTGKTTLVL	110	
RESULT 11				
ABP45301	ID	ABP45301 standard; Protein; 249 AA.		
XX	AC	ABP45301;		
XX	XX	19-AUG-2002 (first entry)		
XX	DE	Human BlyS binding scFv SEQ ID 1312.		
XX	XX	BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;		
KW	KW	tumour necrosis factor; B cell proliferation; B cell differentiation;		
KW	KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;		
KW	KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;		
KW	KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;		
XX	XX	common variable immunodeficiency; acquired immunodeficiency syndrome.		
OS	XX	Homo sapiens.		
XX	XX	WO200202641-A1.		
XX	XX	10-JAN-2002.		
XX	XX	15-JUN-2001; 2001WO-US19110.		
XX	XX	16-JUN-2000; 2000US-212210P.		
PR	PR	17-OCT-2000; 2000US-240816P.		
PR	PR	16-MAR-2001; 2001US-276248P.		
PR	PR	21-MAR-2001; 2001US-277379P.		
PR	PR	25-MAY-2001; 2001US-293499P.		
XX	XX	(HUMA-) HUMAN GENOME SCI INC.		
PA	PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
XX	XX	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;		
XX	XX	WPI; 2002-114799/15.		
PT	PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for		
XX	XX	the diagnosis and treatment of cancers and immune disorders -		
PS	PS	Claim 1; Page 1968-1969; 3148pp; English.		
XX	XX	This invention describes novel antibodies that immunospecifically bind to		
CC	CC	B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the		
CC	CC	tumour necrosis factor (TNF) super family and induces B cell		
CC	CC	proliferation and differentiation. The antibodies of the invention have		
CC	CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,		
CC	CC	antirheumatic and antiAIDS activity and can be used in vaccines to		
CC	CC	inhibit the expression and activity of BlyS. The antibodies bind to BlyS		
CC	CC	and so may be used to detect and quantitate the presence of BlyS in		
CC	CC	biological samples and may be used in this way to diagnose disease		
CC	CC	associated with aberrant expression of BlyS. They may also be		
CC	CC	administered to treat diseases associated with aberrant BlyS expression		
CC	CC	and activity such as cancer, immune, and autoimmune disorders and		
CC	CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,		
CC	CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and		
CC	CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent		
CC	CC	the antibodies and fragments of the antibodies described in the method		
CC	CC	of the invention.		

RESULT 13
AAB67622 standard; Protein; 245 AA.
ID AAB67622 standard; Protein; 245 AA.
AC AAB67622;
XX
DT 29-MAY-2001 (first entry)
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_6.
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX Homo sapiens.
XX WO200114558-A1.
XX 01-MAR-2001.
XX 28-AUG-2000; 2000WO-EP08388.
XX 26-AUG-1999; 99EP-0116691.
XX (MORP-) MORPHOSYS AG.
XX Kretschmar T, Tesar M, Marget M, Kroenke M;
XX WPI; 2001-218451/22.
XX Novel isolated human immunoglobulin or functional immunoglobulin
XX fragment specific for human leukocyte antigen Cw6, useful for treatment
XX of humans and for human leukocyte antigen phenotyping
XX Claim 3; Fig 1; 23pp; English.
XX
XX AAB67617-23 represent single chain antibody (scFv) fragments which
XX are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
XX derived from a synthetic human combinatorial antibody library based on
XX molecular consensus frameworks and CDRs randomised with trinucleotides.
XX The specification describes a human immunoglobulin fragments specific
XX for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
XX studies of natural killer cell silencing as well as miscarriages.
XX HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
XX Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
XX fragments are useful for the preparation of a pharmaceutical for the
XX treatment of humans. They are also useful for HLA phenotyping.
XX Sequence 245 AA;
Query Match 56.0%; Score 315.5; DB 22; Length 245;
Best Local Similarity 60.7%; Pred. No. 1.8e-18;
Matches 65; Conservative 10; Mismatches 29; Indels 3; Gaps 2;
QY 2 LTQPSVSANPGETVKITCSGGSGVAGSYVYQKAPASAPVTIYDNTNRPSPR 61
DB 141 LTQPPSVAVPQQTARISCGDA--LGDKYASWTQOK--PGQAPVLYVYDSDRSGIPER 197
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSSYVGIAGTTLTVL 108
DB 198 FSGNSGNTALTITSGTQADEADYQCQSYDSDSYLVFGGTKTLTVL 244
RESULT 14
ABP45545 standard; Protein; 251 AA.
ID ABP45545 standard; Protein; 251 AA.
AC ABP45545;
XX
DT 19-AUG-2002 (first entry)
DE Human BlyS binding scFv SEQ ID 1556.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX WO200202641-A1.
XX 10-JAN-2002.
XX 15-JUN-2001; 2001WO-US19110.
XX 16-JUN-2000; 2000US-212210P.
XX 17-OCT-2000; 2000US-240816P.
XX 16-MAR-2001; 2001US-276248P.
XX 21-MAR-2001; 2001US-277379P.
XX 25-MAY-2001; 2001US-293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders
XX Claim 1; Page 2259-2261; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX Sequence 251 AA;
Query Match 56.0%; Score 315; DB 23; Length 251;
Best Local Similarity 58.3%; Pred. No. 2e-18;
Matches 63; Conservative 14; Mismatches 29; Indels 2; Gaps 2;
QY 2 LTQPSVSANPGETVKITCSGGSGVAGSYVYQKAPASAPVTIYDNTNRPSPR 61
DB 144 VTQPPAVSAAPGQKVTISCGSSNSIGSYVYVWYQ--LPTAPKLIYDNDKRPSPR 202
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSSYVGIAGTTLTVL 108
DB 203 FSVSKSGTSTLALTITGLQTDGADYICGTWDSLSAGVFGGTKTVL 250
RESULT 15
ABP45829 standard; Protein; 251 AA.
ID ABP45829 standard; Protein; 251 AA.
XX ABP45829
AC ABP45829;
XX

Dt 19-AUG-2002 (first entry)

Kw Human Blys binding scFv SEQ ID 1840.

Ln

Bk Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunopressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.
WO200202641-A1.
10-JAN-2002.

15-JUN-2001; 2001WO-US19110.

16-OCT-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
PR
21-MAR-2001; 2001US-276248P.
PR
21-MAR-2001; 2001US-277379P.
PR
23-MAY-2001; 2001US-293499P.
XX
(HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

WPI; 2002-114799/15.

Pf Antibodies against B Lymphocyte Stimulating polypeptides, useful for
the diagnosis and treatment of cancers and immune disorders -

Claim 1; Page 2597-2598; 3148pp; English.

Sq This invention describes novel antibodies that immunospecifically bind to
B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
tumour necrosis factor (TNF) super family and induces B cell
proliferation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
antirheumatic and antiAIDS activity and can be used in vaccines to
inhibit the expression and activity of Blys. The antibodies bind to Blys
and so may be used to detect and quantitate the presence of Blys in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of Blys. They may also be
administered to treat diseases associated with aberrant Blys expression
and activity such as cancer, immune, and autoimmune disorders and
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID), and
acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
of the invention.

Tm Sequence 251 AA;

Xg

Zo Query Match 56.08; Score 315; DB 23; Length 251;
Best Local Similarity 58.3%; Pred. No. 2e-18;
Matches 63; Conservative 14; Mismatches 29; Indels 2; Gaps 2

Qy 2 LTQPSSVSNAPGPEVKITCSGGSYAGSYYGWYOOKAPASAPVPVIYDNTNRPSNIPSR 61
 :|||:||| ||: |:||||| |::||| ||||| |::::| ::||| :||| :||| ||| ||| |:
Db 144 VTQPPAAVAAPGORVTIISCGSSNNIGSYYSWTQQ-LPGTAPAKLLIIDNDKRPSPIDR 202
 :|||:||| ||: |:||||| |::||| ||||| |::::| ::||| :||| :||| ||| ||| |:

Oy 62 FSGSLGSSTNLTTTGTVQVEADAVYYCGSFDSY-VGITLGAQTTLTLVL 108
 :|||:||| ||: |:||||| |::||| ||||| |::::| ::||| :||| :||| ||| ||| |:

Db 203 FSWSKSQSLSLATLGLTGTDEADNYCYCTWDSSLNSAGVFEGGTKYTFL 250
 :|||:||| ||: |:||||| |::||| ||||| |::::| ::||| :||| :||| ||| ||| |:

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OM protein - protein search, using sw model

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459.831 Million cell updates/sec

Title: US-10-083-424A-26
Perfect score: 563
Sequence: 1 ALTOPSSVSANPGETVKITC.....GSFSSYVILGAGTTLTVL 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	449.5	79.8	126	3	US-08-751-359-12
2	449.5	79.8	126	4	US-08-907-146-12
3	434	77.1	229	3	US-08-751-359-22
4	434	77.1	229	4	US-08-907-146-22
5	426.5	75.8	126	3	US-08-751-359-11
6	426.5	75.8	126	4	US-08-907-146-11
7	426	75.7	125	3	US-08-751-359-13
8	426	75.7	125	4	US-08-907-146-13
9	423.5	75.2	124	3	US-08-751-359-14
10	423.5	75.2	124	4	US-08-907-146-14
11	326.5	58.0	108	4	US-09-025-769B-20
12	318	56.5	111	3	US-08-983-607-35
13	309	54.9	109	3	US-09-157-370-5
14	305	54.2	110	1	US-08-199-911-2
15	305	54.2	114	3	US-09-240-274-62
16	304	54.0	112	4	US-09-025-769B-18
17	304	54.0	234	4	US-09-372-425A-4
18	303.5	53.9	143	2	US-08-345-321-8
19	301	53.5	108	1	US-08-360-125-12
20	301	53.5	108	2	US-08-450-578-12
21	301	53.5	108	2	US-09-017-628-12
22	301	53.5	108	2	US-09-014-880-12
23	301	53.5	108	4	US-08-450-363-12
24	300	53.3	109	1	US-08-478-039-91
25	300	53.3	109	1	US-08-476-349A-91
26	300	53.3	111	2	US-08-958-201-12
27	300	53.3	235	3	US-09-049-672A-10

28	298.5	53.0	112	3	US-08-983-607-31	Sequence 31, Appl
29	297	52.8	245	4	US-10-039-785-47	Sequence 47, Appl
30	296	52.6	111	2	US-08-958-201-14	Sequence 14, Appl
31	296	52.6	112	4	US-09-025-769B-19	Sequence 19, Appl
32	295	52.4	113	1	US-08-211-202-112	Sequence 112, Appl
33	295	52.4	245	4	US-10-039-785-45	Sequence 45, Appl
34	294	52.2	109	3	US-09-240-274-61	Sequence 61, Appl
35	294	52.2	111	2	US-08-665-202-43	Sequence 43, Appl
36	294	52.2	111	4	US-09-315-574-43	Sequence 43, Appl
37	294	52.2	245	4	US-10-039-785-43	Sequence 43, Appl
38	293.5	52.1	110	3	US-09-240-274-63	Sequence 63, Appl
39	293	52.0	111	2	US-08-665-202-36	Sequence 36, Appl
40	293	52.0	111	4	US-09-315-574-36	Sequence 36, Appl
41	293	52.0	234	3	US-08-487-550-2	Sequence 2, Appl
42	293	52.0	234	4	US-09-526-098-2	Sequence 2, Appl
43	293	52.0	258	2	US-08-665-202-5	Sequence 5, Appl
44	293	52.0	258	4	US-09-315-574-5	Sequence 5, Appl
45	293	52.0	262	4	US-09-069-821-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-751-359-12
; Sequence 12, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-12

Query Match 79.8%; Score 449.5; DB 3; Length 126;
Best Local Similarity 82.7%; Pred. No. 4.9e-35;
Matches 91; Conservative 6; Mismatches 6; Indels 7; Gaps 2;
QY 1 ALTOPSSVSANPGETVKITCSGGSVAGSYVYGYOQKAPASAPVTVIYDNTNRPNSIPS 60
|||||
Db 22 ALTOPSSVSANPGETVKITCSG-----GSMYGYOQKAPGSPVTLIYNSQRPDSIPS 76
|||||

```
QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108
Db 77 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 126

RESULT 2
US-08-907-146-12
; Sequence 12, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/907,146
; APPLICATION NUMBER: 08/751,359
; PRIORITY INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLGY: linear
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,359
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLGY: linear
; US-08-907-146-12

Query Match 79.8%; Score 449.5; DB 4; Length 126;
Best Local Similarity 82.7%; Pred. No. 4.9e-35;
Matches 91; Conservative 6; Mismatches 6; Indels 7; Gaps 2;

QY 1 ALTPSSVSANPGETVKITCGSGGYSAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60
Db 22 ALTPSSVSANPGETVKITCGSGGYSAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60
QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108
Db 77 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 126

RESULT 3
US-08-751-359-22
; Sequence 22, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/907,146
; APPLICATION NUMBER: 08/751,359
; PRIORITY INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLGY: linear
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,359
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLGY: linear
; US-08-751-359-22

Query Match 77.1%; Score 434; DB 3; Length 229;
Best Local Similarity 82.6%; Pred. No. 2.7e-33;
Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

QY 1 ALTPSSVSANPGETVKITCGSGGYSAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60
Db 22 ALTPSSVSANPGETVKITCGSGGYSAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60
QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108
Db 77 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 126

RESULT 4
US-08-907-146-22
; Sequence 22, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/907,146
; APPLICATION NUMBER: 08/751,359
; PRIORITY INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLGY: linear
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,359
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLGY: linear
; US-08-751-359-22
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APPLICATION NUMBER: 08/751,359
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-907-146-22

Query Match 77.1%; Score 434; DB 4; Length 229;
Best Local Similarity 82.6%; Pred. No. 2.7e-33;
Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

QY 1 ALTOPSSVSANPGTGVKTCGGGSGYAGSYGGYQOKAPASAPVTVIYDNTNRPSNIPS 60
DB 22 ALTOPSSVSANPGTGVKTCGGDRS-----YGGYQOKAPASAPVTVIYDNTNRPSDIPS 76
QY 61 RFSGSLSGSTNTLTITGVQVDEAVYCGSFD-SSYVGILGAGTTLTVL 108
DB 77 RFSGSKSGSTATLTITGVQADDEAVYCGSADSSSTAGIFGAGTTLTVL 125

RESULT 5
US-08-751-359-11
Sequence 11, Application US/08751359
Patent No. 6143559
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: Concurrently Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-751-359-11

Query Match 75.8%; Score 426.5; DB 3; Length 126;

Best Local Similarity 80.0%; Pred. No. 6.9e-33;
Matches 88; Conservative 2; Mismatches 13; Indels 7; Gaps 2;
QY 1 ALTOPSSVSANPGTGVKTCGGGSGYAGSYGGYQOKAPASAPVTVIYDNTNRPSNIPS 60
DB 22 ALTOPSSVSANPGTGVKTCGGSS-----YGGYQOKAPASAPVTVIYDNTNRPSNIPS 76
QY 61 RFSGSLSGSTNTLTITGVQVDEAVYCGSFDSSSYV--GILGAGTTLTVL 108
DB 77 RFSGSKSGSTATLTITGVRADNNAVYCASTDSSSTAXGIFGAGTTLTVL 126

RESULT 6
US-08-907-146-11
Sequence 11, Application US/08907146
Patent No. 6316600
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,146
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-907-146-11

Query Match 75.8%; Score 426.5; DB 4; Length 126;
Best Local Similarity 80.0%; Pred. No. 6.9e-33;
Matches 88; Conservative 2; Mismatches 13; Indels 7; Gaps 2;
QY 1 ALTOPSSVSANPGTGVKTCGGGSGYAGSYGGYQOKAPASAPVTVIYDNTNRPSNIPS 60
DB 22 ALTOPSSVSANPGTGVKTCGGSS-----YGGYQOKAPASAPVTVIYDNTNRPSNIPS 76
QY 61 RFSGSLSGSTNTLTITGVQVDEAVYCGSFDSSSYV--GILGAGTTLTVL 108
DB 77 RFSGSKSGSTATLTITGVRADNNAVYCASTDSSSTAXGIFGAGTTLTVL 126

RESULT 7
US-08-751-359-13
Sequence 13, Application US/08751359

ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
-COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: Concurrently Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
- TELEPHONE: 512/418-3000
- TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-14

Query Match 75.2%; Score 423.5; DB 3; Length 124;
Best Local Similarity 76.9%; Pred. No. 1.3e-32;
Matches 83; Conservative 6; Mismatches 14; Indels 5; Gaps 1;

QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYQOKAPASAPVTIYDNTNRPNSIPS 60
DQ 22 ALTOPASVSANPGETVEITCSGDSS-----YGYQOKAPASAPVTIYDNTNRPNSIPS 76

QY 61 RFSGLSGSTNTLTITGVQVDEAVYVCGSFDSSVYVGLGAGTTLTVL 108
DQ 77 RFSKSGSTALTITGVQVDEAVYVCGSFDSSVYVGLGAGTTLTVL 124

RESULT 10
US-08-907-146-14
; Sequence 14, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,146
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-907-146-14

Query Match 75.2%; Score 423.5; DB 4; Length 124;
Best Local Similarity 76.9%; Pred. No. 1.3e-32;
Matches 83; Conservative 6; Mismatches 14; Indels 5; Gaps 1;

QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYQOKAPASAPVTIYDNTNRPNSIPS 60
DQ 22 ALTOPASVSANPGETVEITCSGDSS-----YGYQOKAPASAPVTIYDNTNRPNSIPS 76

QY 61 RFSGLSGSTNTLTITGVQVDEAVYVCGSFDSSVYVGLGAGTTLTVL 108

Db 77 RFSKSGSTALTITGVQVDEAVYVCGSFDSSVYVGLGAGTTLTVL 124

RESULT 11
US-09-025-769B-20
; Sequence 20, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-20

Query Match 58.0%; Score 326.5; DB 4; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.3e-23;
Matches 69; Conservative 7; Mismatches 28; Indels 3; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGYQOKAPASAPVTIYDNTNRPNSIPS 61
DQ 3 LTQPPSVSVAPGTARITCSGDS--LGSKYASWYQK-PQAPVLYIDDNKRPSGIPER 59

QY 62 FSGSLSGSTNTLTITGVQVDEAVYVCGSFDSSVYVGLGAGTTLTVL 108
DQ 60 FSGNSGNTALTITSGVQAEADYVCGSWDSSGNVVFSGGTLTVL 106

RESULT 12
US-08-983-607-35
; Sequence 35, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; bodies

```

; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scfv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V373
; FEATURE:
; NAME/KEY: light chain
; US-08-983-607-35

Query Match 56.5%; Score 318; DB 3; Length 111;
Best Local Similarity 59.6%; Pred. No. 8.1e-23;
Matches 65; Conservative 12; Mismatches 30; Indels 2; Gaps 2;

QY 1 ALTOPSSVSANPGETVKITCGSGSYAGSYGWTQKAPASAPVTVIYDNTNRPSNIPS 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 ALTOPPSVSAPGQKVTISCGSSNIGNNVSWY-QLPGTAPKLLIYENKRRPSGIPD 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 RFSGSLSGSTNLTITGVQVEDEAVYYCGSFDSSVVG-ILGAGTTLTVL 108
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 RFSGSKSGTSATLITGLQAEDEAGYVCQSDSSLSGVTGKTLTVL 110
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
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; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-157-370-5

Query Match 54.9%; Score 309; DB 3; Length 109;
Best Local Similarity 61.7%; Pred. No. 5.5e-22;
Matches 66; Conservative 10; Mismatches 27; Indels 4; Gaps 3;

QY 2 LTQPSVSANPGETVKITCGSGSYAGSYGWTQKAPASAPVTVIYDNTNRPSNIPS 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 LTQPPSVSVSPGQTVTISCGDS--LGTCYVSWYQK-PGQAPKLVYDDNRRPSGIPDR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 FSGSLSGSTNLTITGVQVEDEAVYYCGSFDSSVVGILGAGTTLTVL 108
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 FSGSKSGTASLTISGLQAEDEADYYCQSDSSSV-VFGGTTKLTVL 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-08-199-911-2
; Sequence 2, Application US/08199911
; Patent No. 5495002
; GENERAL INFORMATION:
; APPLICANT: Kofrin, Barry J.
; APPLICANT: Haspel, Martin V.
; TITLE OF INVENTION: Tumor Associated Monoclonal Antibody
; TITLE OF INVENTION: 123AV16
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AKZO NOBEL
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,911
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,517
; FILING DATE: 21-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/636,179
; FILING DATE: 31-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/302,155
; FILING DATE: 25-JAN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/697,078
; FILING DATE: 31-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/575,533
; FILING DATE: 31-JAN-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
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Search completed: September 3, 2003, 12:18:25
Job time : 10.9375 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 12:10:30 ; Search time 20.0625 Seconds
(without alignments)
739.130 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 ALTOPSSVSANPGETVKITC.....GSPDSSYVIGILGAGTTTLVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

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2	418.5	74.3	105	15	US-10-083-424-32
3	401	71.2	108	15	US-10-083-424-30
4	394	70.0	104	15	US-10-083-424-28
5	384.5	68.3	104	15	US-10-083-424-40
6	318	56.5	249	11	US-09-880-748-1312
7	315	56.0	251	11	US-09-880-748-1556
8	315	56.0	251	11	US-09-880-748-1840
9	312	55.4	106	15	US-10-269-805-8
10	312	55.4	255	11	US-09-880-748-1156
11	310	55.1	258	11	US-09-880-748-1260
12	309.5	55.0	111	15	US-10-269-805-54
13	309.5	55.0	217	11	US-09-972-656-88
14	309	54.9	123	15	US-10-153-437-6
15	308	54.7	109	15	US-10-001-934-44

16	308	54.7	245	15	US-10-151-882-15	Sequence 15, Appl
17	308	54.7	248	11	US-09-880-748-861	Sequence 861, App
18	308	54.7	258	11	US-09-880-748-1029	Sequence 1029, Ap
19	307.5	54.6	111	15	US-10-269-805-6	Sequence 6, Appli
20	307	54.5	110	15	US-10-269-805-58	Sequence 58, Appl
21	307	54.5	111	15	US-10-199-908-4	Sequence 4, Appli
22	306.5	54.4	245	11	US-09-880-748-1864	Sequence 1864, Ap
23	306.5	54.4	252	11	US-09-880-748-1549	Sequence 1549, Ap
24	306.5	54.4	252	11	US-09-880-748-1992	Sequence 1992, Ap
25	306	54.4	246	11	US-09-880-748-2077	Sequence 2077, Ap
26	306	54.4	253	11	US-09-880-748-1859	Sequence 1859, Ap
27	306	54.4	256	11	US-09-880-748-1015	Sequence 1015, Ap
28	305.5	54.3	253	11	US-09-880-748-1375	Sequence 1375, Ap
29	305	54.2	109	15	US-10-001-934-50	Sequence 50, Appl
30	305	54.2	114	11	US-09-848-798-62	Sequence 62, Appl
31	305	54.2	248	11	US-09-880-748-1995	Sequence 1995, Ap
32	305	54.2	249	11	US-09-880-748-1572	Sequence 1572, Ap
33	305	54.2	249	11	US-09-880-748-1573	Sequence 1573, Ap
34	305	54.2	250	11	US-09-880-748-1565	Sequence 1565, Ap
35	305	54.2	250	11	US-09-880-748-1566	Sequence 1566, Ap
36	305	54.2	252	11	US-09-880-748-1208	Sequence 1208, Ap
37	304	54.0	109	15	US-10-001-934-52	Sequence 52, Appl
38	304	54.0	254	11	US-09-880-748-1139	Sequence 1139, Ap
39	304	54.0	255	11	US-09-880-748-857	Sequence 857, App
40	303.5	53.9	252	11	US-09-880-748-988	Sequence 988, App
41	303.5	53.9	253	11	US-09-880-748-909	Sequence 909, App
42	303.5	53.9	253	11	US-09-880-748-1125	Sequence 1125, Ap
43	303.5	53.9	256	11	US-09-880-748-1301	Sequence 1301, Ap
44	303	53.8	112	15	US-10-269-805-10	Sequence 10, Appl
45	303	53.8	251	11	US-09-880-748-1538	Sequence 1538, Ap

ALIGNMENTS

RESULT 1

US-10-083-424-26
; Sequence 26, Application US/10083424
; Publication No. US20030104497A1

GENERAL INFORMATION:

; APPLICANT: Avicore Biotechnology Institute Inc.

; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Respo

; FILE REFERENCE: for Coccidiosis

; CURRENT APPLICATION NUMBER: US/10/083,424

; CURRENT FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: KR 2001-52934

; PRIOR FILING DATE: 2001-08-30

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: KopatentIn 1.71

; SEQ ID NO 26

; LENGTH: 108

; TYPE: PRT

; ORGANISM: chicken hybridoma cell line 2-1

US-10-083-424-26

Query Match 100.0%; Score 563; DB 15; Length 108;

Best Local Similarity 100.0%; Pred No. 5.6e-48;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALTOPSSVSANPGETVKITCSGGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 1 ALTOPSSVSANPGETVKITCSGGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPS 60

Qy 61 RFGSLSGSTNTLTITGVQVDEAVYICGGSFSDSSYVIGILGAGTTTLVL 108

Db 61 RFGSLSGSTNTLTITGVQVDEAVYICGGSFSDSSYVIGILGAGTTTLVL 108

RESULT 2

US-10-083-424-32

; Sequence 32, Application US/10083424

; Publication No. US20030104497A1

RESULT 8
US-09-880-748-1840
; Sequence 1840, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:

RESULT 10
US-09-880-748-1156
; Sequence 1156, Application US/09880748
; Publication No. US20030059937A1

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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1156
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1156

Query Match      55.4%; Score 312; DB 11; Length 255;
Best Local Similarity 60.2%; Pred. No. 6.1e-23;
Matches 65; Conservative 11; Mismatches 30; Indels 2; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSNIPSR 61
Db 148 LTQPPSVSAPGQKVTISCSGISNIGNKYVSWYQQ-LPGTAPKLLIYDNDKRGIPDR 206

QY 62 FSGSLSGSTNLTITGQVEDEAVYCGSFDSY-VGILGAGTTLTVL 108
Db 207 FSGSKGTSATLGTGLTQDEADYCGTWDSSLSAGVFGGKTLTVL 254

RESULT 11
US-09-880-748-1260
; Sequence 1260, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1260
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1260

Query Match      55.1%; Score 310; DB 11; Length 258;
Best Local Similarity 59.3%; Pred. No. 9.8e-23;
Matches 64; Conservative 12; Mismatches 30; Indels 2; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSNIPSR 61
Db 151 LTQPPSVSAPGQKVTISCSGISNIGNKYVSWYQQ-LPGTAPKLLIYDNDKRGIPDR 209

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QY -62 FSGSLSGSTNLTITGQVEDEAVYCGSFDSYVG-ILGAGTTLTVL 108
Db 210 FSGSKGTSATLGTGLTQDEADYCGANDSSLSAYVFGSGTKTLTVL 257

RESULT 12
US-10-269-805-54
; Sequence 54, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 54
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-54

Query Match      55.0%; Score 309.5; DB 15; Length 111;
Best Local Similarity 57.8%; Pred. No. 4.1e-23;
Matches 63; Conservative 12; Mismatches 31; Indels 3; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSNIPSR 61
Db 4 LTQPPSVSAPGQKVTISCSGSSNIGNNYVSWYQH-LPGTAPKLLIYDNTNRPSGVPDR 62

QY 62 FSGSLSGSTNLTITGQVEDEAVYCGSFDSYVG--ILGAGTTLTVL 108
Db 63 FSGSKGTSASLAIAGLQAEADYICQSYDSSLSGLVFGGKTLTVL 111

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RESULT 13
US-09-972-656-88
; Sequence 88, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 88
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-88

Query Match      55.0%; Score 309.5; DB 11; Length 217;
Best Local Similarity 56.0%; Pred. No. 9e-23;
Matches 61; Conservative 16; Mismatches 29; Indels 3; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSNIPSR 61
Db 4 LTQPHSVSPGKVTITCSGSGSIASHYVQVQOR-PGSAFTNVIYEDKERPSGVPDR 62

QY 62 FSGSLSGSTN--TLTITGQVEDEAVYCGSFDSYVGTLGAGTTLTVL 108
Db 63 FSGSIDSTNGASLTISGLKTEADYICQSYDSSNQWVFGGKTLTVL 111

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RESULT 14
US-10-153-437-6

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; Sequence 6, Application US/10153437
; Publication No. US20030124631A1
; GENERAL INFORMATION:
; APPLICANT: Pier, Gerald B.
; APPLICANT: Preston, Michael J.
; APPLICANT: Cavacini, Lisa
; APPLICANT: Posner, Marshall
; TITLE OF INVENTION: P. aeruginosa Mucoid Exopolysaccharide Specific Binding Peptides
; FILE REFERENCE: B00801/70250
; CURRENT APPLICATION NUMBER: US/10/153,437
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/292,365
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-437-6

Query Match          54.9%; Score 309; DB 15; Length 123;
Best Local Similarity 58.3%; Pred. No. 5.2e-23;
Matches 63; Conservative 14; Mismatches 29; Indels 2; Gaps 2;

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Db      16 LTQPPSVSANPGQRTVISCSSGNLGNFVSWYQQ-LPGAAPRLLIYDNDKRPSPGIPDR 74
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QY      62 FSGSLSGSTNTLTITGQVDEAVYYCGSFDSYVVG-ILGAGTTLTVL 108
      ||||| ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      75 FSGSKSGTSATLIGTLQGTDEADYYCGTWDSSLTAYVFGSGTKVTVL 122
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RESULT 15
US-10-001-934-44
; Sequence 44, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/001,934
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-44

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Best Local Similarity 57.9%; Pred. No. 5.7e-23;
Matches 62; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

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QY      62 FSGSLSGSTNTLTITGQVDEAVYYCGSFDSYVVGILGAGTTLTVL 108
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Db      63 FSGSKSGTSASLAITGLQSEDEADYYCQSYDLT-MGVFGGGKTLTVL 108
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Job time : 21.0625 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 12:02:19 ; Search time 24.4688 Seconds
(without alignments)
1138.991 Million cell updates/sec

Title: US-10-083-424A-26
Perfect score: 563
Sequence: 1 ALTOPSSVSANPGTQKTC.....GSPDSSVYGILGAGTTLTVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	54.2	110	4	Q8TE63
2	300	53.3	233	4	Q8TEC9
3	297.5	52.8	112	4	Q96JDI
4	296.5	52.7	107	4	Q9UL82
5	295	52.4	237	4	Q8WUK4
6	294	52.2	233	4	Q8N5F4
7	292	51.9	116	4	Q96JDI
8	290	51.5	107	4	Q9NSD6
9	289	51.3	237	4	Q8WUK6
10	288.5	51.2	234	4	Q8N355
11	288.5	51.2	236	4	Q96E61
12	288	51.2	112	4	Q96JDI
13	275.5	48.9	236	4	Q8NEJ1
14	267	47.4	101	4	Q8IZD8
15	256.5	45.6	108	4	Q96SB0
16	242	43.0	233	4	Q96I69

17	237	42.1	235	11	Q99M11	Q99M11 mus musculus
18	234	41.6	113	11	O8CGS1	O8CGS1 mus musculus
19	223	39.6	114	11	O8K1F1	O8K1F1 mus musculus
20	222	39.4	112	11	O8K1F3	O8K1F3 mus musculus
21	221	39.3	106	5	Q9U410	Q9U410 schistosoma
22	221	39.3	134	11	O8VDD0	O8VDD0 mus musculus
23	220	39.1	97	11	O9ET13	O9ET13 mus musculus
24	218	38.7	109	11	O9ET13	O9ET13 mus musculus
25	215	38.2	112	11	O8K1F2	O8K1F2 mus musculus
26	212	37.7	107	4	O8UL81	O8UL81 homo sapien
27	211.5	37.6	129	11	O8VDE2	O8VDE2 mus musculus
28	206.5	36.7	108	4	Q9UL70	Q9UL70 homo sapien
29	206	36.6	109	4	Q9UL78	Q9UL78 homo sapien
30	205.5	36.5	108	4	Q9UL77	Q9UL77 homo sapien
31	205	36.4	112	11	O8K1F0	O8K1F0 mus musculus
32	204	36.2	101	11	Q9JL78	Q9JL78 mus musculus
33	204	36.2	107	4	Q96SA9	Q96SA9 homo sapien
34	198	35.2	109	4	Q9UL86	Q9UL86 homo sapien
35	194.5	34.5	234	4	O8NEK1	O8NEK1 homo sapien
36	192.5	34.2	108	4	Q9UL83	Q9UL83 homo sapien
37	192	34.1	109	4	Q9UL85	Q9UL85 homo sapien
38	192	34.1	235	11	Q9JL12	Q9JL12 mus musculus
39	190.5	33.8	109	6	Q9N0W5	Q9N0W5 oryctolagus
40	190.5	33.8	214	11	Q9RIA5	Q9RIA5 mus musculus
41	190.5	33.8	240	4	Q8WUK3	Q8WUK3 homo sapien
42	188.5	33.5	108	4	Q9UL79	Q9UL79 homo sapien
43	184.5	32.8	298	11	O9QYF0	O9QYF0 mus musculus
44	183.5	32.6	109	11	Q920E6	Q920E6 mus musculus
45	180.5	32.1	234	11	O8R062	O8R062 mus musculus

ALIGNMENTS

RESULT 1

Q8TE63 PRELIMINARY; PRT; 110 AA.
ID Q8TE63
AC Q8TE63;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95007525; PubMed=7923137;
RA Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT "Establishment, molecular rescue, and expression of 123AV16-1, a tumor-reactive human monoclonal antibody.";
RL Cancer Res. 54:5178-5185(1994).
DR EMBL; L33985; AAL68704.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 599D1628F8F5437C CRC64;

Query Match 54.2%; Score 305; DB 4; Length 110;
Best Local Similarity 56.9%; Pred. No. 3.le-22;
Matches 62; Conservative 14; Mismatches 31; Indels 2; Gaps 2;

QY 1 ALTOPSSVSANPGTQKTCGGSGYAGSYGYYGQKAPASAPVTVIYDNTNRPSNIPS 60
Db 3 ALTPQPEVSAPGQKVTICSSNIGNNEFVSQQ-FPGAPKLLIYDNNKRPSPVDP 61
QY 61 RFSGSLSGSTNTLTITGVQVEDEAVYCGSFDSY-VGILGAGTTLTVL 108

QY 62 FSGSLGSGTNTLTITGVQVEDEAVYCGSFSS--YVGLGAGTTLTVL 108
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 59 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHAFVGGGTKLTVL 106

RESULT 9

Q8WTU6 ID Q8WTU6 PRELIMINARY; PRT; 237 AA.
AC Q8WTU6; 51.3%; Score 289; DB 4; Length 237;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP NCBI_TaxID=9606;
RC TISSUE=Tonsil;
RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022098; RAH22098.1; -
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;

Query Match
Best Local Similarity 51.3%; Score 289; DB 4; Length 237;
Matches 61; Conservative 14; Mismatches 31; Indels 4; Gaps 3;

QY 2 LTPSSVSANPGETVKITCGSGGSYAGS--YYGYOQKAPASAPVTVYDNTNRPSNIPS 60
Db 23 LTPPPSVGAPGQVTVISCTGSSNIGAGYVHWYQQ-LPGTAPKLLIYGNRPSGVDP 81
QY 61 RFSGSLGSGTNTLTITGVQVEDEAVYCGSFSS--YVGLGAGTTLTVL 108
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 82 RFSGSKSGTSASLAITGLQAEADYYCQSYDLSASGVFGGTKLTVL 131

RESULT 10

Q8N355 ID Q8N355 PRELIMINARY; PRT; 234 AA.
AC Q8N355; 51.3%; Score 288.5; DB 4; Length 236;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-MAR-2003 (TremBLrel. 22, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP NCBI_TaxID=9606;
RC TISSUE=Brain;
RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028090; AAN28090.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match
Best Local Similarity 51.2%; Score 288.5; DB 4; Length 234;
Matches 63; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 2 LTPSSVSANPGETVKITCGSGGSYAGS--YYGYOQKAPASAPVTVYDNTNRPSNIPS 61
Db 23 LTPPPSVGAPGQVTVISCTGSSNIGAGYVHWYQQ-LPGTAPKLLIYGNRPSGVDP 79
QY 62 RFSGSLGSGTNTLTITGVQVEDEAVYCGSFSS--YVGLGAGTTLTVL 108
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 80 FSGNSGNTATLTISRVDAGDEADYYCQLWDSSDHPVVGSGTKLTVL 128

RESULT 11

Q96E61 ID Q96E61 PRELIMINARY; PRT; 236 AA.
AC Q96E61; 51.2%; Score 288.5; DB 4; Length 236;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP NCBI_TaxID=9606;
RC TISSUE=Brain;
RA Strausberg R.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match
Best Local Similarity 55.0%; Pred. No. 3.1e-20;
Matches 60; Conservative 15; Mismatches 31; Indels 3; Gaps 3;

QY 2 LTPSSVSANPGETVKITCGSGGSYAGS--YYGYOQKAPASAPVTVYDNTNRPSNIPS 60
Db 23 LAQPPSVGAPGQVTVISCTGSSNIGAGYVHWYQQ-FPGAAPKLLIYGNRPSGVDP 81
QY 61 RFSGSLGSGTNTLTITGVQVEDEAVYCGSFSSYVG-ILGAGTTLTVL 108
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 82 RFSGSKSGTSASLAITGLQAEADYYCQSYDLSASGVFGGTKLTVL 130

RESULT 12

Q96JD2 ID Q96JD2 PRELIMINARY; PRT; 112 AA.
AC Q96JD2; 51.2%; Score 288.5; DB 4; Length 236;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Anyloid lambda 6 light chain variable region NEG (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RESULT 14	
ID	Q81ZD8
AC	PRELIMINARY; PRT; 101 AA.
DT	Q81ZD8;
DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Anti-thyroglobulin light chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Jang Y.-J., Chung J., Park J.-Y.;
RT	"Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT	Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY145444; AAN64328.1; -
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Jang Y.-J., Chung J., Park J.-Y.;
RT	"Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT	Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY145444; AAN64328.1; -
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=93375893; PubMed=9712075;
RT	Aderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT	"Molecular analysis of polyclonal antibodies from
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT	antibody v region genes";
RT	J. Immunol. 161:2020-2031(1998).
DR	EMBL; U96394; AAB68783.1; -
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
Query Match 45.6%; Score 256.5; DB 4; Length 108;	
Best Local Similarity 51.0%; Pred. No. 1.6e-17;	
Matches 50; Conservative 14; Mismatches 33; Indels 1; Gaps 1;	
QY 2 LTQPSVSNANPETVKITCSGGGSYAGSYVGYGQQKAPASAPVTVIYDNTNRPSNIPSR 61	

Db ||||| | ||: | |:|||| | || | |||| | :|| | ||| :||
4 LTQPPASGTPGQRTISCSSNIGSNVYVYQO-LFGTAPKLLIYRNQRPSPGVDR 62
QY ||||| ||: | |:|||| | || | |||| | :|| | ||| :||
62 FSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSSYVGIL 99
Db ||||| ||: | |:|||| | || | |||| | :|| | ||| :||
63 FSGSKGTSASLAISGRSEDEADYYCAAWDDRLSGFM 100

Search completed: September 3, 2003, 12:14:47
Job time : 25.4688 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:02:54 ; Search time 9.28125 Seconds
(without alignments)
1119.054 Million cell updates/sec

Title: US-10-083-424A-26
Perfect score: 563
Sequence: 1 ALTPSSVSANPGETVKITC.....GSFDSVYVILGAGTTTLVL 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434	77.1	125	2 A31493	Ig light chain pre
2	430	76.4	213	2 A21177	Ig light chain pre
3	419.5	74.5	230	2 S49449	Ig lambda chain -
4	403.5	71.7	113	1 L1CHV	Ig lambda chain pr
5	386.5	68.7	97	2 I51216	Ig light chain var
6	317	56.3	235	2 S05270	Ig lambda chain pr
7	313	55.6	111	2 S47009	Ig lambda chain V1
8	311	55.2	111	1 L1HUNG	Ig lambda chain V-
9	307	54.5	130	1 L1HUGL	Ig lambda chain pr
10	306	54.4	131	2 S24321	Ig lambda chain pr
11	302.5	53.7	120	2 S30525	Ig lambda chain V
12	302	53.6	105	2 S49533	Ig lambda chain V
13	301	53.5	119	2 S30526	Ig lambda chain V
14	300	53.3	231	2 S25751	Ig lambda chain -
15	299	53.1	107	1 L4HUHL	Ig lambda chain V-
16	299	53.1	111	2 S38497	Ig lambda chain -
17	299	53.1	111	2 S47185	Ig lambda chain -
18	298	52.9	130	2 S09712	Ig lambda chain V
19	297.5	52.8	110	2 S36272	Ig lambda chain V
20	297	52.8	113	2 A29700	Ig lambda chain V
21	295.5	52.5	112	1 L6HUAR	Ig lambda chain V-
22	295	52.4	106	1 L4HUBU	Ig lambda chain V-
23	295	52.4	111	2 S36274	Ig lambda chain V
24	295	52.4	235	2 S25758	Ig lambda chain -
25	294.5	52.3	111	2 S44105	Ig lambda chain V-
26	294	52.2	112	2 S19664	Ig lambda chain V
27	294	52.2	232	2 S25742	Ig lambda chain -
28	294	52.2	235	2 S25759	Ig lambda chain -
29	293.5	52.1	232	2 S25756	Ig lambda chain -

30	293	52.0	108	2 S47184	Ig lambda chain -
31	293	52.0	109	2 S19663	Ig lambda chain V
32	292.5	52.0	131	1 L6HUEB	Ig lambda chain pr
33	292	51.9	108	2 S38498	Ig lambda chain -
34	291.5	51.8	112	2 S31515	Ig lambda chain V
35	291.5	51.8	112	2 S51148	antibody light cha
36	291	51.7	127	2 S70444	Ig lambda chain pr
37	291	51.7	231	2 S25738	Ig lambda chain -
38	290	51.5	109	1 L1HUEP	Ig lambda chain V-
39	290	51.5	111	2 S46397	Ig lambda chain V
40	289.5	51.4	112	2 S46395	Ig lambda chain V
41	289	51.3	111	2 S36263	Ig lambda chain V-
42	288	51.2	111	1 L2HUNI	Ig lambda chain V-
43	287	51.0	111	1 L2HUBH	Ig lambda chain V-
44	287	51.0	111	1 L6HULT	Ig lambda chain V-
45	287	51.0	120	2 S30527	Ig lambda chain V

ALIGNMENTS

RESULT 1

A31493
Ig light chain precursor V region - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 21-Jan-2000
C:Accession: A31493
R:McCormack, W.T.; Tjoelker, L.W.; Carlson, L.M.; Petryniak, B.; Barth, C.F.; Hum
Cell 56, 785-791, 1989
A:Title: Chicken IgL gene rearrangement involves deletion of a circular episome a
A:Reference number: A31493; MUID:89168419; PMID:2493991
A:Accession: A31493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <MCC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:34-106/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 434; DB 2; Length 125;
Best Local Similarity 82.6%; Pred. No. 3.3e-31;
Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

Qy	1	ALTPSSVSANPGETVKITCSGGSVAGSYGYGYQOKAPASAPVTVIYDNTNRPSNIPS	60
Db	22	ALTPSSVSANPGETVKITCSGDRS-----YGYQOKAPASAPVTVIYANTNRPSDIPS	76
Qy	61	RFSGSLSGSTNLTITGTGQVDEAVYYCGSFD--SSYVGILGAGTTTLVL	108
Db	77	RFSGSKSGSTATLTITGVOADDEAVYYCGSADSSAGIFGAGTTTLVL	125

RESULT 2

A21177
Ig light chain precursor V-J region - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C:Accession: A21177; B22327
R:Reynaud, C.A.; Dahan, A.; Weill, J.C.
Proc. Natl. Acad. Sci. U.S.A. 80, 4099-4103, 1983
A:Title: Complete sequence of a chicken lambda light chain immunoglobulin derived
A:Reference number: A21177; MUID:83247424; PMID:6408641
A:Accession: A21177
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-213 <REY>
A:Cross-references: GB:K00678; NID:q212159; PIDN:AAA48906.1; PID:g212160
R:Reynaud, C.A.; Anquez, V.; Dahan, A.; Weill, J.C.
Cell 40, 283-291, 1985
A:Title: A single rearrangement event generates most of the chicken immunoglobulin
A:Reference number: A30861; MUID:85099341; PMID:3917859
A:Accession: B22327
A:Molecule type: DNA

```

-21/Domain: signal sequence #status predicted <SIG>

```

Reference number: S04601; MUID:89296497; PMID:2500644

Query Match 55.2%; Score 311; DB 1; Length 111; Best Local Similarity 59.3%; Pred. No. 1.7e-20; Matches 64; Conservative 12; Mismatches 30; Indels 2; Gaps 2;

QY 2 LTQPSSVSNANPGETVKITCGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSPISR 61 ||||| ||||| :||| | : ||||| | : ||||| ||||| ||||| ||||| Db F:15-91/Dmain: immunoglobulin homology <IMM> F:/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) F:22-89/Disulfide bonds: #status predicted

QY 62 FSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSY-VGILGAGTTTLTVL 108 ||||| ||||| :||| | : ||||| ||||| ||||| ||||| ||||| Db F:SGSKSGTSATLGITGLQTGDEADYYCGTWDSLSVGMEGGTRTVL 110

RESULT 9 LIHUBL Ig lambda chain precursor V-I region (BL2) - human C:Species: Homo sapiens (man) C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999 C:Accession: A01966 R:Tsuji moto, Y.; Croce, C.M. Nucleic Acids Res. 12, 8407-8414, 1984 A:Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence A:Reference number: A01966; MUID:85062823; PMID:6095199 A:Accession: A01966 A:Molecule type: mRNA A:Residues: 1-130 <TSU> A:CROSS-references: GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087 C:Genetics: A:Gene: GDB:IGLV@ A:CROSS-references: GDB:l19342; OMIM:l47240 A:Map position: 22q11.2-22q11.2 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate in dimers. C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin F:1-19/Domain: signal sequence #status predicted <SIG> F:20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT> F:20-115/Region: V segment F:34-110/Domain: immunoglobulin homology <IMM> F:116-130/Region: J segment F:41-108/Disulfide bonds: #status predicted

Query Match 54.5%; Score 307; DB 1; Length 130; Best Local Similarity 58.3%; Pred. No. 4.4e-20; Matches 63; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

QY 2 LTQPSSVSNANPGETVKITCGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSPISR 61 ||||| ||||| :||| | : ||||| | : ||||| ||||| ||||| ||||| Db LTQPPSVAAAPQGKVTISCGSSNGINDVYSWYQQ-VPGTAPKLLIYDNNKRPSGIPDR 81 ||||| ||||| :||| | : ||||| ||||| ||||| ||||| |||||

QY 62 FSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVG-ILGAGTTTLTVL 108 ||||| ||||| :||| | : ||||| ||||| ||||| ||||| ||||| Db F:SGSKSGTSATLGITGLQTGDEADYYCGTNNSLSGWVFGGKTTLTVL 129

RESULT 10 S24321 Ig lambda chain precursor - human C:Species: Homo sapiens (man) C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C:Accession: S24321 R:Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Biochem. J. 285, 149-152, 1992 A:Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain reference number: S24319; MUID:92344562; PMID:1379039 A:Accession: S24321

Job time : 10.2812 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:01:44 ; Search time 4.96875 Seconds
(without alignments)
1022.165 Million cell updates/sec

Title: US-10-083-424A-26
Perfect score: 563
Sequence: 1 ALTOPSSVSANPGTIVKTC.....GSFSSVVGILGAGTTLVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	403.5	71.7	113	1	LV1_CHICK
2	311	55.2	111	1	LV1D_HUMAN
3	307	54.5	130	1	LV1G_HUMAN
4	299	53.1	107	1	LV1C_HUMAN
5	295.5	52.5	112	1	LV1A_HUMAN
6	295	52.4	106	1	LV4A_HUMAN
7	292.5	52.0	131	1	LV6E_HUMAN
8	290	51.5	109	1	LV1I_HUMAN
9	288	51.2	111	1	LV2B_HUMAN
10	287	51.0	111	1	LV2C_HUMAN
11	287	51.0	111	1	LV2D_HUMAN
12	286	50.8	109	1	LV2E_HUMAN
13	286	50.8	111	1	LV6C_HUMAN
14	285	50.6	106	1	LV4E_HUMAN
15	284	50.4	111	1	LV2A_HUMAN
16	280	49.7	111	1	LV2D_HUMAN
17	279.5	49.6	112	1	LV2K_HUMAN
18	279	49.6	111	1	LV2F_HUMAN
19	279	49.6	111	1	LV3B_HUMAN
20	277.5	49.3	110	1	LV2J_HUMAN
21	277	49.2	108	1	LV3A_HUMAN
22	277	49.2	109	1	LV1F_HUMAN
23	272	48.3	106	1	LV4B_HUMAN
24	272	48.3	111	1	LV2H_HUMAN
25	268	47.6	111	1	LV1C_HUMAN
26	267	47.4	106	1	LV4D_HUMAN
27	267	47.4	111	1	LV2I_HUMAN
28	265	47.1	111	1	LV2G_HUMAN
29	262.5	46.6	112	1	LV6B_HUMAN
30	261	46.4	111	1	LV2L_HUMAN
31	259.5	46.1	112	1	LV1B_HUMAN
32	257	45.6	108	1	LV5A_HUMAN
33	254.5	45.2	112	1	LV1H_HUMAN

34	253	44.9	111	1	LV7A_HUMAN	P01720	homo sapien
35	244	43.3	111	1	LV1A_HUMAN	P01699	homo sapien
36	231	41.0	103	1	LV1E_HUMAN	P01703	homo sapien
37	228	40.5	108	1	KV6K_MOUSE	P04945	mus musculus
38	223.5	39.7	129	1	LV1B_MOUSE	P01724	mus musculus
39	221.5	39.3	110	1	LV1C_MOUSE	P01725	mus musculus
40	217.5	38.6	129	1	LV1D_MOUSE	P01727	mus musculus
41	215	38.2	117	1	LV0A_HUMAN	P04211	homo sapien
42	213.5	37.9	129	1	LV1D_MOUSE	P01726	mus musculus
43	211	37.5	107	1	KV6G_MOUSE	P04941	mus musculus
44	210	37.3	107	1	KV6F_MOUSE	P04940	mus musculus
45	210	37.3	107	1	KV6H_MOUSE	P04942	mus musculus

ALIGNMENTS

RESULT 1
LV1_CHICK
ID LV1_CHICK STANDARD: PRT: 113 AA.
AC P04210;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-1 region precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509341; PubMed=3917859;
RA Reynaud C.A., Anquez V., Dahan A., Weill J.-C.;
RT "A single rearrangement event generates most of the chicken
immunoglobulin light chain diversity.";
RL Cell 40:283-291(1985).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M12317; AAA50793.1;
CC PIR: A01992; LICHV.
CC HSSP: P80748; 2LOI.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF000047; Ig; 1.
CC SMART: SM00406; IgV; 1.
CC PROSITE: PSS0835; IG_LIKE; 1.
CC Immunoglobulin v region; Signal.
CC
CC SIGNAL 1 21
CC CHAIN 22 113
CC DOMAIN 22 41
CC COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 42 49
CC COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 50 65
CC COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 66 72
CC COMPLEMENTARITY-DETERMINING-4.
CC DOMAIN 73 104
CC COMPLEMENTARITY-DETERMINING-5.
CC DISULFID 105 113
CC BY SIMILARITY.
CC
CC NON_TER 113 113
CC SEQUENCE 113 AA; 11695 MW; 167BA8FA9449733B CRC64;
Query Match 71.7%; Score 403.5; DB 1; Length 113;
Best Local Similarity 85.1%; Pred. No. 4e-32;
Matches 80; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

OY 1 ALTOPSSVSANPGTIVKTCGGGSGGSGYAGSYGYYGWYQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSGDRS-----YGYGQKAPGADPTLIYDNTNRPSNIPS 76
Qy 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS 94
Db 77 RFGSKSGSATLTITGVQADDEAVYCGSADSS 110

RESULT 2

LV1G_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX MEDLINE=83186114; PubMed=6404900;
RA Kameitani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
immunoglobulins. IV. Assignment of a subgroup.",
RL J. Biochem. 93:421-429(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; LIHUNG.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 105 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 55.2%; Score 311; DB 1; Length 111;
Best Local Similarity 59.3%; Pred. No. 3e-23;
Matches 64; Conservative 12; Mismatches 30; Indels 2; Gaps 2;

Qy 2 LTQPSVSANPGETVKITCSGGSAGSYGYGQKAPASAPVTVIYDNTNRPSNIPS 61
Db 4 LTQPPVSAPGQEVITSCSSSNGDVFVSWYQO-LPGTAPKLLIYDNNKRPSPGIPDR 62
Qy 62 FGSLSGSNTLTITGVQVEDEAVYCGSFDSSY-VGILGAGTTLTVL 108
Db 63 FSGSKSGTSATLTITGLTGDEADYCGTWDSLSVGMFGGGRVTVL 110

RESULT 3

LV1G_HUMAN STANDARD; PRT; 130 AA.
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01147; CAA25598.1; -
DR PIR; A01986; LIHUBL.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BBI7D3A55EBF CRC64;
Query Match 54.5%; Score 307; DB 1; Length 130;
Best Local Similarity 58.3%; Pred. No. 8.6e-23;
Matches 63; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

Qy 2 LTQPSVSANPGETVKITCSGGSAGSYGYGQKAPASAPVTVIYDNTNRPSNIPS 61
Db 23 LTQPPVSAPGQEVITSCSSSNGDVFVSWYQO-VGTAPKLLIYDNNKRPSPGIPDR 81
Qy 62 FGSLSGSNTLTITGVQVEDEAVYCGSFDSSYVG-ILGAGTTLTVL 108
Db 82 FSGSKSGTSATLTITGLTGDEADYCGTWDSLSGWSGVTGKTLTVL 129

RESULT 4
LV4C_HUMAN STANDARD; PRT; 107 AA.
ID LVAC_HUMAN
AC P01717;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-IV region Hil.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX MEDLINE=78187276; PubMed=418804;
RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
RT "Amino acid sequence of the variable region of the light (lambda)
chain from human myeloma cryoimmunoglobulin IgG Hil.";
RL Biochemistry 17:1718-1723(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
CC IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
CC 135-ILE (HIL NUMBERING) INSTEAD OF VAL.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

```
DR PIR; A01983; L4HUHL.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig_V.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 97 IG-LIKE.  
FT NON_TER 107 107  
SQ SEQUENCE 107 AA; 11517 MW; A5C8AFFE0C0C590A CRC64;  
  
Query Match 53.1%; Score 299; DB 1; Length 107;  
Best Local Similarity 60.7%; Pred. No. 4.le-22;  
Matches 65; Conservative 10; Mismatches 28; Indels 4; Gaps 4;  
  
QY 2 LTQPSVSNPGETVKITCSGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
Db 4 LTQPSVSNPGETVKITCSGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 60  
  
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFDSSYVIGLGAGTTTLTVL 108  
Db 61 FSSSTSGTTLTISGVAEADYCYQAWDNS-ASIFGGGKTLTVL 106  
  
RESULT 5  
LV6A_HUMAN STANDARD; PRT; 112 AA.  
AC P01721;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-VI region AR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE (AMYLOID PROTEIN AR).  
RX MEDLINE=82091000; PubMed=6797401;  
RA Sletten K., Natvig J.B., Husby G., Juul J.;  
RT "The complete amino acid sequence of a prototype  
immunoglobulin-lambda light-chain-type amyloid-fibril protein AR.";  
RL Biochem. J. 195:561-572(1981).  
CC -!- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING  
FROM THIS PROTEIN.  
CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A  
PATIENT WITH AMYLOIDOSIS.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01987; L6HUR.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_V.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
KW Immunoglobulin V region; Amyloid.  
FT DOMAIN 1 107 IG-LIKE.  
FT NON_TER 112 112  
SQ SEQUENCE 112 AA; 11918 MW; 570BCD9A368EF1FE CRC64;  
  
Query Match 52.5%; Score 295.5; DB 1; Length 112;  
Best Local Similarity 55.5%; Pred. No. 9.2e-22;  
Matches 61; Conservative 19; Mismatches 25; Indels 5; Gaps 4;
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QY 2 LTQPSVSNPGETVKITCSGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 60  
Db 4 LTQPSVSNPGETVKITCSGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
  
QY 61 FSGSLSGSTN--TLTITGVQVEDEAVYCGSFDSSYVIGLGAGTTTLTVL 108  
Db 62 FSGSIDDSANSASLTISGLKTEADYCYQSYNSHHVYVFGGKTKTVL 111  
  
RESULT 6  
LV4A_HUMAN STANDARD; PRT; 106 AA.  
AC P01715;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region Bau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059189; PubMed=4435717;  
RA Baczko K., Braun D., Hilschmann N.;  
RT "Pattern of antibody structure, the primary structure of monoclonal  
immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones  
protein Bau).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01981; L4HUBU.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_V.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 102 IG-LIKE.  
FT NON_TER 106 106  
SQ SEQUENCE 106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;  
  
Query Match 52.4%; Score 295; DB 1; Length 106;  
Best Local Similarity 58.9%; Pred. No. 9.7e-22;  
Matches 63; Conservative 10; Mismatches 30; Indels 4; Gaps 3;  
  
QY 2 LTQPSVSNPGETVKITCSGSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
Db 3 LTQPSLSVSPQTASITCS--GDKLGEYVQWYQOK-PQGSPLVIYHDSKRPSPGIPER 59  
  
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFDSSYVIGLGAGTTTLTVL 108  
Db 60 FSGSNSGTATLTISGTQAMDEADYCYQAWD-SYTVIFGGGKTLTVL 105  
  
RESULT 7  
LV6E_HUMAN STANDARD; PRT; 131 AA.  
AC P06319;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-VI region EB4 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]
```

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SEQUENCE FROM N.A.
RA MEDLINE=85215660; PubMed=3923440;
RA Anderson M.I.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
RT expressed in the Burkitt's lymphoma cell line EB4.";
RL Nucleic Acids Res. 13:2931-2941(1985).
DR PIR; A01900; LSHUEP.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EB4.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 110 FRAMEWORK-3.
FT DOMAIN 111 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 131 FRAMEWORK-4.
FT DISULFID 41 110 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

Query Match 52.0%; Score 292.5; DB 1; Length 131;
Best Local Similarity 53.2%; Pred. No. 2.1e-21;
Matches 58; Conservative 17; Mismatches 31; Indels 3; Gaps 2;

QY 2 LTQPSVSSANPGETVKITCSGGSYAGSYGYHQKAPASAPVTVIYDNTNRPSNIPSR 61
DB 23 LTQPHSVSPGKTVITISCTSGSIASNYQVQQR-VSAPTIVIEDNQRLGVPDR 81

QY 62 FSGSLSGSTNTLTITGVQVEAEVYCGSFSSVYVILGAGTTLTVL 108
DB 82 FSGSIDSSNSASLTISGLKTEADYQCQFDTNQVFGGKTLTVL 130

RESULT 8
LV11_HUMAN STANDARD; PRT; 109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86000126; PubMed=3929803;
RA Toft K.G., Sletten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda).";
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC -1- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC PEPTIDES WERE POSTIONED BY HOMOLOGY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A24656; LIHUEP.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DOMAIN 1 105 IG-LIKE.
FT CARBOHYD 104 104 N-LINKED (GLCNAc. . .).
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;

Query Match 51.5%; Score 290; DB 1; Length 109;
Best Local Similarity 53.3%; Pred. No. 3e-21;
Matches 57; Conservative 17; Mismatches 31; Indels 2; Gaps 2;

QY 2 LTQPSVSSANPGETVKITCSGGSYAGSYGYHQKAPASAPVTVIYDNTNRPSNIPSR 61
DB 4 LTQPPSLSAAPGQRVSISCSGSSNIGKNYVDWYQQ-LPTAPKLLIFNNKRPSPGIPDR 62

QY 62 FSGSLSGSTNTLTITGVQVEAEVYCGSFSSVYVILGAGTTLTVL 108
DB 63 FSGSKSGTSATLGTITGLTQGTDEAIYCGTWNRR-SVFGGNTVTIV 108

RESULT 9
LV2B_HUMAN STANDARD; PRT; 111 AA.
AC P01705;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region NEI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72233223; PubMed=5043326;
RA Garver F.A., Hilschmann N.;
RT "The primary structure of a monoclonal human lambda-type
RT immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL Eur. J. Biochem. 26:10-32(1972).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01970; L2HUNI.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; Glycoprotein;
KW Pyrolidone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAc. . .).
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 51.2%; Score 288; DB 1; Length 111;
Best Local Similarity 52.3%; Pred. No. 4.8e-21;
Matches 57; Conservative 19; Mismatches 31; Indels 2; Gaps 2;

QY 1 ALTPQSSVSNPGETVKITCSGGSYAGSYGYHQKAPASAPVTVIYDNTNRPSNIP 59
DB 3 ALTPQASVSGSPGQISITICTGTSYGVNFVSWYQON-PGKAPKLMIEGKRPSPGV 61

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RA	Dwulet F.E., Strako K., Benson M.D.;
RT	"Amino acid sequence of a lambda VI primary (AL) amyloid protein
RL	(WLT).";
DR	Scand. J. Immunol. 22:653-660(1985).
DR	PIR; A01989; L6HULT.
DR	HSSP; P01709; 2MCG.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig_1.
DR	SMART; SM00406; Igv; 1.
DR	PROSITE; PS0835; IG_LIKE; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 22
FT	DOMAIN 23 35
FT	DOMAIN 36 50
FT	DOMAIN 51 57
FT	DOMAIN 58 91
FT	DOMAIN 92 101
FT	DOMAIN 102 111
FT	DISULFID 22 91
FT	NON_TER 111 111
SEQ	SEQUENCE 111 AA; 11966 MW; 0C8B2FE37BCE24F CRC64;
	Query Match 51.0%; Score 287; DB 1; Length 111;
	Best Local Similarity 54.1%; Pred. No. 6e-21;
	Matches 59; Conservative 17; Mismatches 29; Indels 4; Gaps 3;
QY	2 LTQPSSVSANPGETVKITCSGGSYAGSYGYGYYQQKAPASAPVTIYDNTVRPSNIPSR 61
DB	4 LTQLPLVSGSPKPTTICTGTSSGSIGSNVQVYQQR-PGSAPTNNVIENNQRPSVPDR 62
QY	62 FSGLSLGSSTN-TLTIQTGVQEENAVYICGSFDSYVGILCAGTTTLVL 108
DB	63 FSGSIDSSNSASLTISGLKTEADYICQSYDNHNHVFG-GTRLTTLVL 110
	: : :: : :
	: : :: : :
	: : :: : :
RESULT 12	
LV2E_HUMAN	
ID	LV2E_HUMAN STANDARD; PRT; 109 AA.
AC	P01708;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig lambda chain V-II region BUR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE.
RA	MEDLINE=80006606; PubMed=113407;
RX	Infante A.J., Putnam F.W.;
RT	"Primary structure of a human IgAl immunoglobulin. V. Amino acid
RT	sequence of a human IgA lambda light chain (Bur).";
RL	J. Biol. Chem. 234:9006-9016(1979).
CC	-1- MTSCELLANEUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC	MARKERS.
CC	-1- MTSCELLANEUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A01974; L2HUHR.
DR	HSSP; P01709; 2MCG.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig_1.
DR	SMART; SM00406; Igv; 1.

63 FSGSIDRSSNSASLTISGLQTEADYYCQSYDRDH-WVFGGTKLTVL 110

RT	"Primary structure of cryo Bence-Jones protein (Tog) from the urine
RT	of a patient with IgD myeloma.";
RL	Mol. Immunol. 16:439-444(1979).
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC	PIR; A01369; L2HUGT.
DR	DR HSP; P01709; 2MCG.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_Like; 1.
KW	Immunoglobulin v region: Bence-Jones protein;
KW	Pyrrolidone carboxylic acid.
FT	DOMAIN 1 100 IG-LIKE.
FT	MOD_RES 1 1
FT	DISULFID 22 90 PYRROLIDONE CARBOXYLIC ACID.
FT	NON_TER 111 111 BY SIMILARITY.
SQ	SEQUENCE 111 AA; 111713 MW; FD20AEF4CE5364E2 CRC64;

Query Match	50.4%	Score 284;	DB 1;	Length 111;
Best Local Similarity	53.2%;	pred. No. 1.2e-20;		
Matches	58;	Conservative 29;	Mismatches 29;	Indels 2; Gaps 2;
QY	1	ALTQPSSVSNAPGETVKITCGSGGGSVAGSY-YGWTTQQKAPASAPVTIVTDNTRRPSNP	59	
Db		: : : : : : : : :		
	3	ALTQPASVSASPQSITISCTGTNDIGSYSVYSWTQQ-YPGRAKPKVLIEDVNSRPSPGV	61	
QY	60	SRSFGLSSTNLTIWTVGOVEDEANYICGFSDSSVYGILCAGTTLTVL	108	
Db		: : : : : : : :		
	62	HREFGSKGNATSLTISLGQAEDAHFYCSYTSSTGTFIFGGGYTVFWL	110	

Search completed: September 3, 2003, 12:10:20
Job time : 6.96875 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:09:30 ; Search time 174.656 Seconds
(without alignments)
538.192 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 ALTOPSSVSANPGETVKITC.....GSPDSSVVGILGAGTTTLVL'108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PTCUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
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- 18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
- 19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
- 22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
- 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
- 31: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	563	100.0	108	26	US-10-083-424-26
2	563	100.0	108	26	US-10-083-424A-26

3	481.5	85.5	257	1	PCT-US02-29003A-57	Sequence 57, Appl
4	481.5	85.5	257	1	PCT-US02-29003B-57	Sequence 57, Appl
5	463.5	82.3	102	22	US-09-791-537-87221	Sequence 87221, A
6	459.5	81.6	269	23	US-09-830-779-9	Sequence 9, Appl
7	452.5	80.4	102	22	US-09-791-537-129881	Sequence 129881, A
8	450	79.9	105	22	US-09-791-537-86163	Sequence 86163, A
9	449.5	79.8	245	22	US-09-791-537-139118	Sequence 139118, A
10	449	79.8	246	22	US-09-791-537-130347	Sequence 130347, A
11	447	79.4	116	22	US-09-791-537-151022	Sequence 151022, A
12	443	78.7	103	22	US-09-791-537-87234	Sequence 87234, A
13	439	78.0	106	22	US-09-791-537-87166	Sequence 87166, A
14	434	77.1	125	22	US-09-791-537-44409	Sequence 44409, A
15	434	77.1	229	22	US-09-791-537-139316	Sequence 139316, A
16	434	77.1	234	22	US-09-791-537-129944	Sequence 129944, A
17	432	76.7	244	22	US-09-791-537-130346	Sequence 130346, A
18	432	76.7	244	22	US-09-791-537-130378	Sequence 130378, A
19	431.5	76.6	234	22	US-09-791-537-129973	Sequence 129973, A
20	430.5	76.5	119	22	US-09-791-537-81436	Sequence 81436, A
21	430	76.4	108	22	US-09-791-537-86680	Sequence 86680, A
22	430	76.4	108	22	US-09-791-537-86687	Sequence 86687, A
23	430	76.4	213	22	US-09-791-537-44410	Sequence 44410, A
24	429.5	76.3	232	22	US-09-791-537-134932	Sequence 134932, A
25	429	76.2	237	22	US-09-791-537-129974	Sequence 129974, A
26	428	76.0	101	22	US-09-791-537-86714	Sequence 86714, A
27	427.5	75.9	107	22	US-09-791-537-86685	Sequence 86685, A
28	426.5	75.8	258	1	PCT-US02-29003A-55	Sequence 55, Appl
29	426.5	75.8	258	1	PCT-US02-29003B-55	Sequence 55, Appl
30	425.5	75.6	102	22	US-09-791-537-87232	Sequence 87232, A
31	425.5	75.6	253	1	PCT-US02-29003A-51	Sequence 51, Appl
32	425.5	75.6	253	1	PCT-US02-29003A-53	Sequence 53, Appl
33	425.5	75.6	253	1	PCT-US02-29003B-51	Sequence 51, Appl
34	425.5	75.6	253	1	PCT-US02-29003B-53	Sequence 53, Appl
35	424	75.3	103	22	US-09-791-537-87225	Sequence 87225, A
36	423.5	75.2	101	22	US-09-791-537-129942	Sequence 129942, A
37	423.5	75.2	104	22	US-09-791-537-86174	Sequence 86174, A
38	423.5	75.2	253	1	PCT-US02-29003A-1	Sequence 1, Appl
39	423.5	75.2	253	1	PCT-US02-29003A-52	Sequence 52, Appl
40	423.5	75.2	253	1	PCT-US02-29003B-1	Sequence 1, Appl
41	423.5	75.2	253	1	PCT-US02-29003B-52	Sequence 52, Appl
42	423	75.1	101	22	US-09-791-537-86704	Sequence 86704, A
43	423	75.1	101	22	US-09-791-537-86718	Sequence 86718, A
44	423	75.1	101	22	US-09-791-537-87198	Sequence 87198, A
45	423	75.1	108	22	US-09-791-537-86683	Sequence 86683, A

ALIGNMENTS

RESULT 1
US-10-083-424-26
; Sequence 26, Application US/10083424
; GENERAL INFORMATION:
; APPLICANT: Avicore Biotechnology Institute Inc.
; TITLE OF INVENTION: Recombinant Scfv Antibodies Specific to Eimeria spp. Respor
; FILE OF INVENTION: for Coccidiosis
; FILE REFERENCE: Avicore-USA-1
; CURRENT APPLICATION NUMBER: US/10/083,424
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: KR 2001-52934
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: chicken hybridoma cell line 2-1
US-10-083-424-26

Query Match 100.0%; Score 563; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALTOPSSVSANPGETVKITCSGGSGYAGSYIYGWYQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 1 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 60
QY 61 RFSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSYVYVILGAGTTLVL 108
Db 61 RFSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSYVYVILGAGTTLVL 108

RESULT 2

US-10-083-424A-26
; Sequence 26, Application US/10083424A
; GENERAL INFORMATION:
; APPLICANT: Avicore Biotechnology Institute Inc.
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Elmeria spp. Responsible
; FILE REFERENCE: for Coccidiosis
; CURRENT APPLICATION NUMBER: AVICORE-USA-1
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US/10/083,424A
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: KR 2001-52934
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: chicken hybridoma cell line 2-1
US-10-083-424A-26

Query Match 100.0%; Score 563; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 60
Db 1 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 60
QY 61 RFSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSYVYVILGAGTTLVL 108
Db 61 RFSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSYVYVILGAGTTLVL 108

RESULT 3

PCT-US02-29003A-57
; Sequence 57, Application PC/TUS0229003A
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten
; APPLICANT: Forschung e.V.
; APPLICANT: ZHANG, Mei Yun
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: ZIMMERMANN, Sabine
; APPLICANT: DI FIORE, Stefano
; APPLICANT: EMANS, Neil
; APPLICANT: FISCHER, Rainer
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods
; FILE REFERENCE: of Making and Using
; CURRENT APPLICATION NUMBER: PCT/US02/29003A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/318,904
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 57
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scfv N5
PCT-US02-29003A-57

Query Match 85.5%; Score 481.5; DB 1; Length 257;
Best Local Similarity 87.2%; Pred. No. 4.6e-39;
Matches 95; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 60
Db 146 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 205
QY 61 RFSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSYVYVILGAGTTLVL 108
Db 206 RFSGSKSGSTGTLTITGQVQADDEAVYCGSGDSYSSVIGIFGAGTTLVL 254

RESULT 4

PCT-US02-29003B-57
; Sequence 57, Application PC/TUS0229003B
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten
; APPLICANT: Forschung e.V.
; APPLICANT: ZHANG, Mei Yun
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: ZIMMERMANN, Sabine
; APPLICANT: DI FIORE, Stefano
; APPLICANT: EMANS, Neil
; APPLICANT: FISCHER, Rainer
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods
; FILE REFERENCE: of Making and Using
; CURRENT APPLICATION NUMBER: PCT/US02/29003B
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/318,904
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 57
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scfv N5
PCT-US02-29003B-57

Query Match 85.5%; Score 481.5; DB 1; Length 257;
Best Local Similarity 87.2%; Pred. No. 4.6e-39;
Matches 95; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 60
Db 146 ALTPSSVSANPGETVKITCGGSGYAGSYIYGYQOKAPASAPVTIYDNTNRPNSIPS 205
QY 61 RFSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSYVYVILGAGTTLVL 108
Db 206 RFSGSKSGSTGTLTITGQVQADDEAVYCGSGDSYSSVIGIFGAGTTLVL 254

RESULT 5

US-09-791-537-87221
; Sequence 87221, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 87221
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-791-537-87221

Query Match 82.3%; Score 463.5; DB 22; Length 102;

Qy 2 LTQPSVSNPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSPSR 61
Db 1 LTQPSVSNPGETVKITCSGGSDSG---YGTQKSPGAPVTIYINDKRPSNIPSR 57
Qy 62 FSGSLSGSTNLTITGVQVEDEAVYCGSFDSSVYGVILGAGTTLTVL 108
Db 58 FSGSGSTNLTITGVQAEDEAVYFCGNRDSYVGFAGTTLTVL 104

RESULT 10

US-09-791-537-130347
; Sequence 130347, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130347
; LENGTH: 246
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-130347

Query Match 79.8%; Score 449; DB 22; Length 246;
Best Local Similarity 82.2%; Pred. No. 7.3e-36;
Matches 88; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

Qy 2 LTQPSVSNPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSPSR 61
Db 1 LTQPSVSNPGETVKITCSGGSDSG---YGTQKSPGAPVTIYINDKRPSNIPSR 58
Qy 62 FSGSLSGSTNLTITGVQVEDEAVYCGSFDSSVYGVILGAGTTLTVL 108
Db 59 FSGSGSTNLTITGVQAEDEAVYFCGGYGVTDVGMFGAGTTLTVL 105

RESULT 11

US-09-791-537-151022
; Sequence 151022, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 151022
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Gallus gallus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)...(4)
; OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-151022

Query Match 79.48%; Score 447; DB 22; Length 116;
Best Local Similarity 83.3%; Pred. No. 4.8e-36;
Matches 90; Conservative 3; Mismatches 9; Indels 6; Gaps 2;
Qy 1 ALTOPSSVSNPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSPSR 60
Db 14 ALTOPSSVSNPGETVKITCSGDS-----YGYQKSPGAPVTIYDNTNRPSPSR 68

Qy 61 RFSGSLSGSTNLTITGVQVEDEAVYCGSFDSSVYGVILGAGTTLTVL 108
Db 69 RFSGSGSTNLTITGVQAEDEAVYCGGYDSS-SAIFGAGTTLTVL 115

RESULT 12

US-09-791-537-87234
; Sequence 87234, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87234
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-791-537-87234

Query Match 78.7%; Score 443; DB 22; Length 103;
Best Local Similarity 80.6%; Pred. No. 1e-35;
Matches 87; Conservative 7; Mismatches 8; Indels 6; Gaps 2;

Qy 1 ALTOPSSVSNPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSPSR 60
Db 1 ALTOPSSVSNPGETVKITCSGDS-----YGYQKSPGAPVTIYDNTNRPSPSR 55
Qy 61 RFSGSLSGSTNLTITGVQVEDEAVYCGSFDSSVYGVILGAGTTLTV 107
Db 56 RFSGSGSTNLTITGVQAEDEAVYFCGGYEGGTSAGIFGAGTTLTV 103

RESULT 13

US-09-791-537-87166
; Sequence 87166, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87166
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-791-537-87166

Query Match 78.0%; Score 439; DB 22; Length 106;
Best Local Similarity 78.3%; Pred. No. 2.7e-35;
Matches 83; Conservative 10; Mismatches 11; Indels 2; Gaps 1;

Qy 1 ALTOPSSVSNPGETVKITCSGGSYAGSYGGYQKAPASAPVTIYDNTNRPSPSR 60
Db 1 ALTOPASVSNPGETVKITCSGGRYGNYGGYQKSPGAPVTIYDNTNRPSPSR 60
Qy 61 RFSGSLSGSTNLTITGVQVEDEAVYCGSFDSS--YVILGAGTT 104
Db 61 RFSGSPGRTTILLITGVQVEDEAVYCGSFDSSVYGVIFGAGTT 106

RESULT 14

Search completed: September 3, 2003, 12:49:35
Job time : 175.756 secs

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RESULT 11
US-60-485-404-70
; Sequence 70, Application US/60485404
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeh, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-PR
; CURRENT APPLICATION NUMBER: US/60/485,404
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/406,997
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/460,829
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 111
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: VL region of anti-TNF-alpha/Scfv antibody
US-60-485-404-70

Query Match 53.4%; Score 300.5; DB 7; Length 111;
Best Local Similarity 57.8%; Pred. No. 1.4e-16;
Matches 63; Conservative 14; Mismatches 29; Indels 3; Gaps 3;
QY 2 LTQPSSVSANPGETVKITCSGGSYAGS-YYGYQOKAPASAPVTIVYDNTNRPSNIPS 60
DB 4 LTQPSSVSANPGQRTVITCSGSSNIGAGYDWHYQQ-LPGTAPKLLIYNSNRPSGVPD 62
QY 61 RFGSLSGSTNTLTITGVQVEAEVYCGSFSSVYV-ILGAGTTTLTVL 108
DB 63 RFGSKSGTSASLAITGLQAEADYCYQSYDSSLSGSVFGGKTTLVL 111

RESULT 12
US-10-291-265-755
; Sequence 755, Application US/10291265
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 755
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-755

Query Match 53.4%; Score 300.5; DB 6; Length 232;
Best Local Similarity 58.9%; Pred. No. 2.7e-16;
Matches 63; Conservative 10; Mismatches 31; Indels 3; Gaps 2;

QY 2 LTQPSSVSANPGETVKITCSGGSYAGSYYGYQOKAPASAPVTIVYDNTNRPSNIPS 61
DB 23 LTQPSSVSANPGQRTVITCSGDN-LGNKYVAMYYQQA-GQSPVLVIYQDDKRPSEIPER 79
QY 62 FSGSLSGSTNTLTITGVQVEAEVYCGSFSSVYVILGAGTTTLTVL 108
DB 80 FSGNSGNTATLTISGTQAMDEADYCYQADSSVAVFVGSGTKTLTVL 126

RESULT 13
US-10-275-046-77
; Sequence 77, Application US/10275046
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPT
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MS-GPC11 VL
US-10-275-046-77

Query Match 53.3%; Score 300; DB 6; Length 109;
Best Local Similarity 57.0%; Pred. No. 1.5e-16;
Matches 61; Conservative 12; Mismatches 32; Indels 2; Gaps 2;
QY 2 LTQPSSVSANPGETVKITCSGGSYAGSYYGYQOKAPASAPVTIVYDNTNRPSNIPS 61
DB 4 LTQPSSVSANPGQRTVITCSGSSNIGSNYSVWYQQ-LPGTAPKLLIYDNNQRPSPGVPDR 62
QY 62 FSGSLSGSTNTLTITGVQVEAEVYCGSFSSVYVILGAGTTTLTVL 108
DB 63 FSGSKSGTSASLAITGLQSEADYCYQSYDYG-IYVFGGKTTLTVL 108

RESULT 14
US-10-275-046-87
; Sequence 87, Application US/10275046
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPT
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MS-GPC-8-10
US-10-275-046-87

Query Match 53.3%; Score 300; DB 6; Length 111;
Best Local Similarity 56.5%; Pred. No. 1.6e-16;
Matches 61; Conservative 12; Mismatches 33; Indels 2; Gaps 2;
QY 2 LTQPSSVSANPGETVKITCSGGSYAGSYYGYQOKAPASAPVTIVYDNTNRPSNIPS 61
DB 4 LTQPSSVSANPGQRTVITCSGSSNIGSNYSVWYQQ-LPGTAPKLLIYDNNQRPSPGVPDR 62

Search completed: September 3, 2003, 12:54:38
Job time : 8.13125 secs

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OM protein - protein search, using sw model.

Run on: September 3, 2003, 12:00:29 ; Search time 35.6615 Seconds
(without alignments)
547.464 Million cell updates/sec

Title: US-10-083-424A-18
Perfect score: 663
Sequence: 1 AVTLDESGLQTPGALS.....AGCGDIDANGHTEIVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	79.9	146	19	AAW60170
2	507	76.5	129	22	AAW60170
3	496.5	74.9	141	19	AAW60172
4	494.5	74.6	147	19	AAW60173
5	487	73.5	269	21	AAW71010
6	478.5	72.2	145	19	AAW60171
7	403.5	60.9	177	24	ABJ36939
8	401	60.5	138	21	AAJ32406
9	400.5	60.4	253	24	ABJ19830
					Chicken Mab heavy
					Chicken protein #1
					Heavy chain variab
					Heavy chain variab
					Chicken phospholam
					Heavy chain variab
					Anti-CD40 monoclon
					Mouse anti-verotox
					Human VEGF-2 relat

10	399	60.2	384	22	AAW24101
11	395.5	59.7	95	23	ABG60414
12	394	59.4	221	24	ABR01534
13	393.5	59.4	222	24	ABR01515
14	393	59.3	127	22	AAW33584
15	392.5	59.2	224	24	ABR01513
16	392.5	59.2	239	23	ABP46012
17	392.5	59.2	240	22	AAW46051
18	390.5	58.9	122	20	AAW43253
19	390.5	58.9	249	23	ABP45094
20	390.5	58.9	253	20	AAW30225
21	390.5	58.9	258	20	AAW30221
22	390.5	58.9	268	20	AAW30228
23	390.5	58.9	273	20	AAW30224
24	390.5	58.9	556	20	AAW30218
25	390.5	58.9	580	20	AAW30217
26	390	58.8	117	22	AAE12061
27	390	58.8	123	18	AAW15534
28	389.5	58.7	239	23	ABP46011
29	389.5	58.7	247	23	ABP44985
30	388.5	58.6	120	23	AAO18449
31	388.5	58.6	249	23	ABP44881
32	388.5	58.6	249	23	ABP44885
33	388	58.5	125	23	ABG77142
34	387.5	58.4	140	18	AAW13524
35	387.5	58.4	254	23	ABP45690
36	387	58.4	248	23	ABP44902
37	387	58.4	470	23	ABG77158
38	386.5	58.3	118	23	AAO18441
39	386.5	58.3	131	18	AAW13520
40	386.5	58.3	136	24	ABP55473
41	386.5	58.3	240	22	AAW46007
42	386.5	58.3	367	24	ABP55467
43	386	58.2	115	21	AAW39519
44	385.5	58.1	118	23	AAW33803
45	385.5	58.1	118	23	ABW57561

ALIGNMENTS

RESULT 1
AAW60170
ID AAW60170 standard; Protein; 146 AA.

XX AC AAW60170;
XX DT 23-SEP-1998 (first entry)

XX Chicken Mab heavy chain variable domain sequence.

XX Chicken; monoclonal antibody; MAB; immortalisation; immunisation;
KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;
KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
KW transforming growth factor beta; CFTR; TGF beta.

XX Gallus sp.

XX WO9822510-A2.

XX PD 28-MAY-1998.

XX PF 18-NOV-1997; 97WO-US21077.

XX PR 18-NOV-1996; 96US-0751359.

XX (ARCH-) ARCH DEV CORP.

XX (UABR-) UAB RES FOUND.

XX Accavitti MAV, Michael NM, Thompson CB;

XX WPI; 1998-312421/27.

XX

FF Z9-FEB-2000; 2000JP-0054875.

PA (UAB)

XX AC AAY71010;
 XX DT 29-AUG-2000 (first entry)
 XX DE Chicken phospholamban (PLB) antibody, contractilin.
 XX DE Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiomyocyte; transport peptide; penetratin; cargo peptide; chicken;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW cardiant; treatment; heart failure; myocardial dysfunction.
 XX OS Gallus domesticus.
 XX PN WO200025804-A2.
 XX PD 11-MAY-2000.
 XX PE 02-NOV-1999; 99WO-US25692.
 XX PR 02-NOV-1998; 98US-0106718.
 XX PR 27-JUL-1999; 99US-0145883.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 XX PI Scott C, Wang Y, Silverman GJ;
 XX DR WPI; 2000-365393/31.
 XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase
 XX PS Disclosure; Page 50-51; 56pp; English.
 XX CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is that of contractilin protein, a
 CC chicken antibody peptide with hyperactive regions. This is used to raise
 CC polyclonal PLB antibody, by immunising a chicken repeatedly with the
 CC human PLB peptide from the cytoplasmic domain (residues 3-19).
 XX SQ Sequence 269 AA;
 Query Match 73.5%; Score 487; DB 21; Length 269;
 Best Local Similarity 77.0%; Pred. No. 6.6e-35;
 Matches 97; Conservative 6; Mismatches 17; Indels 6; Gaps 3;
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTSSHGMMWVRQTPGKLEWAGISNTGYTYA 61
 DB 129 VTLDSEGGGLQTPGGALSLVCKASGFTSSHGMMWVRQTPGKLEWAGISNTGYTYA 61
 QY 62 PAVKGRATISRDNGSTVRLQINLRADDTGYTCAGKAGYACAG--CGGD-IDAWGHGT 117
 DB 189 AAVKGRATILRDNGSTVRLQIDNLRDPEDATYFCVK--TKCGNGWCCGADRDAWGHGT 246
 QY 118 EVIVSS 123
 DB 247 EVIVSS 252
 RESULT 6
 AAW60171

ID AAW60171 standard; Protein; 145 AA.
 XX AAW60171;
 XX DT 23-SEP-1998 (first entry)
 XX DE Heavy chain variable domain sequence of anti-CFTR 4-9.
 XX DE Chicken; monoclonal antibody; MAB; immortalisation; immunisation;
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
 KW transforming growth factor beta; CFTR; TGF beta.
 XX OS Gallus sp.
 XX PN WO9822510-A2.
 XX PD 28-MAY-1998.
 XX PE 18-NOV-1997; 97WO-US21077.
 XX PR 18-NOV-1996; 96US-0751359.
 XX PA (ARCH-) ARCH DEV CORP.
 XX PI (UABR-) UAB RES FOUND.
 XX PI Accavitti MAV, Michael NM, Thompson CB;
 XX DR WPI; 1998-312421/27.
 XX PT Production of new monoclonal antibodies - by immunising chickens and
 PT immortalising B cells, used for, e.g. diagnosis and passive
 PT treatment of disease
 XX PS Example 2; Page 61; 97pp; English.
 XX CC This represents the amino acid sequence of the heavy chain variable
 CC domain of anti-CFTR 4-9. The invention provides a method for producing
 CC chicken monoclonal antibodies (MAB) against a variety of antigens. The
 CC method comprises immunising a chicken with an antigen and isolating and
 CC immortalising B cells. From a selected antibody-producing B cell,
 CC nucleic acid containing antigen-binding exons of the light and heavy
 CC chain genes is prepared. The heavy and light chain nucleic acid are
 CC cloned separately in vectors that encode the constant and leader
 CC regions of the heavy and light chains. The vectors are transferred to
 CC host cells which are cultured and the MAB is isolated. Such antibodies
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospholipids and
 CC carbohydrates). The MAB can be raised against antigenic determinants that
 CC do not normally induce a response in mammals. The structure of the
 CC chicken immunoglobulin (Ig) gene is such that even after diversification
 CC by repeated gene conversions and maturation, the genomic DNA of the
 CC expressed locus will always have the same L-V (leader-variable) intron
 CC and J (junction)-3', flanking sequences. Thus the sequences flanking the
 CC antigen-binding domain of rearranged chicken genes are known with
 CC certainty, allowing specific amplification with a single set of primers.
 CC The method is particularly used to produce MAB against mammalian antigens
 CC with highly conserved epitopes. The MABs are used for separation,
 CC detection, quantification or removal of antigens, particularly for
 CC diagnosis, including in vivo imaging. They are useful as
 CC immunohistochemical reagents, and for passive treatment of diseases,
 CC such as cystic fibrosis.
 XX SQ Sequence 145 AA;
 Query Match 72.2%; Score 478.5; DB 19; Length 145;
 Best Local Similarity 77.2%; Pred. No. 1.9e-34;
 Matches 98; Conservative 6; Mismatches 18; Indels 5; Gaps 2;
 QY 1 AVTLDSEGGGLQTPGGALSLVCKASGFTSSHGMMWVRQTPGKLEWAGISNTGYTYA 60
 DB 20 AVTLDSEGGGLQTPGGALSLVCKASGFTT-SYLMHWVRQAPGKLEWVGGRSDGSKTGY 78

Qy	62	PVKGRATISRDNCGSTVRQLNNLRADTCTYYCAK--GGAYCACCAGGDDIDAWHGHTVI	120
Db	81	DSVKGREFTISRNSKNLTLYLQMNSLRADETAVYYCAKDGGYYSYGFDYWGQGTLVT	140
Qy	121	VSS	123
Db	141	VSS	143

RESULT 8	
AAV32406	
ID	AAV32406 standard; Protein; 138 AA.
XX	
XX	AAV32406;
XX	
XX	13-MAR-2000 (first entry)
XX	
XX	Mouse anti-verotoxin II antibody VTml-1 humanised VH region.
XX	
KW	Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
KW	monoclonal antibody; heavy chain; mouse; humanised antibody; human;
KW	Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW	HUS; therapy.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
Key	Location/Qualifiers
Peptide	1..19
FT	/note= "signal peptide"
FT	20..138
FT	/note= "mature protein"
FT	50..54
FT	/note= "complementarity determining region 1"
FT	69..85
FT	/note= "complementarity determining region 2"
FT	118..127
FT	/note= "complementarity determining region 3"
XX	
XX	WO9959629-A1.
PN	
XX	
PD	25-NOV-1999.
XX	
XX	19-MAY-1999; 99WO-US11179.
XX	
XX	20-MAY-1998; 98US-0086570.
PR	
XX	
XX	(TEIJ) TEIJIN LTD.
PA	(PROT-) PROTEIN DESIGN LABS INC.
PA	
XX	

Matsumoto I, Imaizumi A, Kimura I, Igakuo I, CO MS, Vasques M;
XX
XX
WPI; 2000-086580/07.
DR
DR N-PSDB; AA235243.
XX
XX
Humanized antibody binding to verotoxin II used for treating Verotoxin
PT
PT producing *E. coli* -
XX
XX
Claim 12; Fig 2a; 59pp; English.
XX
XX
This sequence represents a humanised heavy chain variable region of
CC
CC murine monoclonal antibody Vtm1-1 (MuvTm1-1), an antibody that
CC specifically binds to the B subunit of verotoxin II (VT2). The
CC invention relates to humanised antibodies against VT2 that are capable

of neutralizing V12 and/or V12 variants. The humanised antibody is a CC
CC humanized form of MuVml-1 comprising the complementarity determining CC
CC regions of MuVml-1 and the heavy and light chain variable region CC
CC frameworks from the human GF4 antibody heavy and light chain CC
CC frameworks, provided that at least 1 position selected from L49, H29, CC
CC H30, H49 and H98 is occupied by the amino acid at the equivalent CC
CC position of the MuVml-1 antibody heavy or light chain variable region CC
CC framework. Such humanized antibodies (see AAY32406-07) have an affinity

CC for vnt2 that is 3-, 5 or 10-times that of MuVtm1-1. They are used for
 CC treating a patient suffering from, or at risk of, the toxic effects
 CC from Vt2 (claimed), especially for treating verotoxin producing
 CC Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome
 CC (HUS).
 XX
 SQ

Query Match 60.5%; Score 401; DB 21; Length 138;
 Best Local Similarity 64.8%; Pred. No. 1.1e-27;
 Matches 79; Conservative 12; Mismatches 27; Indels 4; Gaps 1;
 QY 2 VTLDSEGGGLQTPGGLSLVCKASGFTFSSHGMMVVRQTPGKLEWAGISNTGTYTYA 61
 Db 21 VQLVESGGGLVQPGGSLRLCAASGFTFSSYGMVVRQAPGKLEWATISTGGSYTYP 80
 QY 62 PAVKGRATISRDNQSTVRLQLNNLRADTGTTCAGKAYCAGCGGDIIDAWHGTEIV 121
 Db 81 DSVKGRFTISRDNKNTLYLQMSLRADTAVYICARRG-----DAWGNLDYWGQGLTV 136
 QY 122 SS 123
 Db 137 SS 138

RESULT 9

ABJ19830
 ID ABJ19830 standard; Protein; 253 AA.

AC ABJ19830;
 XX

DT 10-APR-2003 (first entry)
 XX

DE Human VEGF-2 related protein SEQ ID NO 76.
 XX

KW Cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic;
 KW antithritic; antidiabetic; ophthalmological; antiallergic;
 KW immunosuppressive; dermatological; antipsoriatic; vulnerrary; antibody;
 KW CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer;
 KW proliferative disorder; cardiovascular disorder; arrhythmia;
 KW cerebrovascular disorder; cerebral anoxia; inflammatory disease;
 KW infectious disease; autoimmune disease; rheumatoid arthritis;
 KW Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;
 KW angiogenesis; wound healing; vascular tissue repair; human.
 XX

OS Homo sapiens.
 XX

PN WO200283704-A1.
 XX

PD 24-OCT-2002.
 XX

PF 12-APR-2002; 2002WO-US11474.
 XX

PR 13-APR-2001; 2001US-283385P.
 XX

PR 24-JAN-2002; 2002US-350366P.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Rosen CA, Albert VR, Ruben SM, Wager RE;
 XX

DR WPI; 2003-092991/08.
 XX

PT New isolated polynucleotide encoding an antibody which inhibits a
 PT VEGF-2 polypeptide, useful for diagnosing, treating or preventing
 PT diseases associated with aberrant VEGF-2 expression or function, e.g.
 PT cancer or inflammation
 XX

PS Disclosure; Page 386-387; 425pp; English.
 XX

CC The invention relates to an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody comprising an
 CC amino acid sequence selected from at least one, two or three CDR
 CC region(s) of a VH or VL domain where the first antibody

CC immunospecifically inhibits a VEGF-2 polypeptide. The isolated
 CC polynucleotide is useful in diagnosing, treating, preventing, prognosing,
 CC ameliorating or monitoring diseases associated with aberrant VEGF-2 or
 CC VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,
 CC such as cancer and other proliferative disorders, cardiovascular
 CC disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral
 CC anoxia), inflammatory diseases, infectious diseases, autoimmune diseases
 CC (e.g. rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),
 CC diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and
 CC antibodies may also be used to stimulate angiogenesis, wound healing, and
 CC promoting vascular tissue repair. The polynucleotide and polypeptide may
 CC also be used for in vitro purposes related to scientific research,
 CC synthesis of DNA and manufacture of DNA vectors, and for the production
 CC of diagnostics and therapeutics to treat human diseases. This sequence
 CC represents a human VEGF-2 related protein of the invention.
 XX

SQ Sequence 253 AA;

Query Match 60.4%; Score 400.5; DB 24; Length 253;
 Best Local Similarity 63.2%; Pred. No. 2.3e-27;
 Matches 79; Conservative 12; Mismatches 31; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGLSLVCKASGFTFSSHGMMVVRQTPGKLEWAGISNTGTYTYA 61
 Db 2 VQLVESGGGLVQPGGSLRLCAASGFTFSSYGMVVRQAPGKLEWATISTGGSYTYA 61

QY 62 PAVKGRATISRDNQSTVRLQLNNLRADTGTTCAGKAYCAGCG---GDIIDAWHGTE 118
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRADTAVYICARRNRYCSTGTCYSDGMDVWGQGLT 121

QY 119 VTSS 123
 Db 122 VTSS 126

RESULT 10

AM24101
 ID AAM24101 standard; Protein; 384 AA.

XX AAM24101;
 AC

DT 12-OCT-2001 (first entry)
 XX

DE Human EST encoded protein SEQ ID NO: 1626.
 XX

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX

OS Homo sapiens.
 XX

PN WO200154477-A2.
 XX

PD 02-AUG-2001.
 XX

PF 25-JAN-2001; 2001WO-US02687.
 XX

PR 25-JAN-2000; 2000US-0491404.
 XX

PR 17-JUL-2000; 2000US-0617746.
 XX

PR 03-AUG-2000; 2000US-0631451.
 XX

PR 15-SEP-2000; 2000US-0663870.
 XX

PA (HYSE-) HYSEQ INC.
 XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 XX

PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX

DR WPI; 2001-476164/51.
 XX

DR N-PSDB; AAH98760.
 XX

PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -

XX PS Claim 20; Page 1102-1103; 1275pp; English.
 XX CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX XX
 XX SQ Sequence 384 AA;

Query Match 60.2%; Score 399; DB 22; Length 384;
 Best Local Similarity 61.4%; Pred. No. 5e-27;
 Matches 81; Conservative 11; Mismatches 30; Indels 10; Gaps 2;
 QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTYA 61
 Db 21 VQLVESGGGLVQPGGSLRLSCLAAAGFTFSSYAMSVVRQAPGKLEWVSGIGSGSSTIYA 80
 QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGTTCYKAG-GAYCAGCGG-----DID 111
 Db 81 DSVKGRFTISRDNSQNTLYLQMNLSRAEDTAVTYCAKSHPAYTYGSGSYSHYYTYGMD 140
 QY 112 AMHGTEVIVSS 123
 Db 141 VMQGTTVTIVSS 152

RESULT 11
 ABG60414
 ID ABG60414 standard; Protein; 95 AA.
 XX AC ABG60414;
 XX DT 30-JUL-2002 (first entry)
 XX DE Selective targeting peptide #89.
 XX KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.
 XX OS Synthetic.
 XX PN WO200220769-A1.
 XX PD 14-MAR-2002.
 XX PF 07-SEP-2001; 2001WO-US27692.
 XX PR 08-SEP-2000; 2000US-231266P.
 XX PR 17-JAN-2001; 2001US-0765101.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Arap W, Pasqualini R;
 XX DR WPI; 2002-415731/44.
 XX PT Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease,
 PT e.g. cancer, inflammatory or autoimmune diseases, infections or
 PT cardiovascular disease -
 XX PS Claim 22; Page 73; 317pp; English.
 XX CC The invention relates to an isolated peptide of 100 amino acids or less

CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting
 CC peptides of the invention.
 XX XX
 XX SQ Sequence 95 AA;

Query Match 59.7%; Score 395.5; DB 23; Length 95;
 Best Local Similarity 87.8%; Pred. No. 2.2e-27;
 Matches 79; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
 QY 1 AVTLDESGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTYV 60
 Db 7 AVTLDESGGGLQTPGGALSIVCKASGFTFSSYPMVVRQAPGKLEWVAVISSGT-TWY 65
 QY 61 APAVKGRATISRDNGQSTVRLQNLNRAED 90
 Db 66 APAVKGRATISRDNGQSTVRLQNLNRAED 95

RESULT 12
 ABR01534
 ID ABR01534 standard; Protein; 221 AA.
 XX AC ABR01534;
 XX DT 16-APR-2003 (first entry)
 XX DE Human anti-TIMP-1 antibody heavy chain #32.
 XX KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
 KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
 KW variable light chain; cystostatic; nephrotropic; cardiant; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX OS Homo sapiens.
 XX PN WO200286085-A2.
 XX PD 31-OCT-2002.
 XX PF 24-APR-2002; 2002WO-US12801.
 XX PR 24-APR-2001; 2001US-285683P.
 XX PA (FARB) BAYER CORP.
 XX PA (MORP-) MORPHOSYS AG.
 XX PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;
 XX DR WPI; 2003-129114/12.
 XX DR N-PSDB; ABZ74805.
 XX PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1)
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 PT hypertrophy or lung cancer -
 XX PS Claim 20; Page 170; 228pp; English.
 XX CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)
 CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine -

XX Claim 1; Column 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,

CC preferably a human antibody, (I) having an amino acid sequence comprising

CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has

CC immunostimulant activity, and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal

CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH8615 to AAH8726 represent the nucleotide sequence which encode

CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy

CC chain CDR3 amino acid sequences which are given in the exemplification

CC of the present invention.

XX Sequence 127 AA;

SQ

Query Match 59.3%; Score 393; DB 22; Length 127;

Best Local Similarity 61.9%; Pred. No. 5e-27;

Matches 78; Conservative 12; Mismatches 32; Indels 4; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTTPGKGLEWVAGISNTGTYTYA 61

DB 2 VQLLESGGGLVQPGGSLRLSCAASGFTFSSYSHWVRQAPGKGLEWVSSISNTIYYA 61

QY 62 PAVKGRATISRDNQGVTRVLQNLNLAEDTGTYYCAKGGAYCAGC---GGDIDAWGHGT 117

DB 62 DAVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDSTRYSNFLRWVRSDGMDVWGOT 121

QY 118 EVIVSS 123

DB 122 TVIVSS 127

RESULT 15

ABR01513

ID ABR01513 standard; Protein: 224 AA.

XX AC ABR01513;

XX DT 16-APR-2003 (first entry)

XX DE Human anti-TIMP-1 antibody heavy chain #11.

XX KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;

XX KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;

XX KW variable light chain; cytosolic; nephrotropic; cardiant; liver fibrosis;

XX KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;

XX KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;

XX KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX OS Homo sapiens.

XX PN WO200286085-A2.

XX PD 31-OCT-2002.

XX PF 24-APR-2002; 2002WO-US12801.

XX PR 24-APR-2001; 2001US-285683P.

XX PA (FARB) BAYER CORP.

XX PA (MORP-) MORPHOSYS AG.

XX PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;

XX DR WPI; 2003-129114/12.

XX DR N-PSDB; AB274784.

XX PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1)

XX PT antibodies for diagnosing or ameliorating the symptoms of a disorder

XX PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate

XX PT hypertrophy or lung cancer

XX Claim 20; Page 155; 228pp; English.

XX The invention relates to a novel purified preparation of a human

CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)

CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of

CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and

CC a variable light chain (VLC)DR3 region. An antibody preparation of the

CC invention has hepatotropic, cytostatic, nephrotropic and cardiant

CC activity. The human antibody is useful for decreasing an MMP-inhibiting

CC activity of a TIMP-1. It is especially useful for ameliorating the

CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver

CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary

CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic

CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon

CC cancer. The antibody is also useful for detecting a TIMP-1 in a test

CC preparation, or in diagnosing a disorder in which a TIMP-1 level is

CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy

CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 224 AA;

SQ

Query Match 59.2%; Score 392.5; DB 24; Length 224;

Best Local Similarity 64.8%; Pred. NO. 1e-26;

Matches 79; Conservative 11; Mismatches 29; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTTPGKGLEWVAGISNTGTYTYA 61

DB 2 VQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGGSTYYA 61

QY 62 PAVKGRATISRDNQGVTRVLQNLNLAEDTGTYYCAKGGAYCAGCGGDIDAWGHGTEVIV 121

DB 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARYMAYMAEA---IDVWGQGTLVTV 118

QY 122 SS 123

DB 119 SS 120

Search completed: September 3, 2003, 12:09:17

Job time : 36.6615 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:03:39 ; Search time 11.3177 Seconds
(without alignments)
459.831 Million cell updates/sec

Title: US-10-083-424A-18

Perfect score: 663

Sequence: 1 AVTLDESGGLQTPGGALSL.....AGCGGDIDAWGHGTEIVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	79.9	146	3 US-08-751-359-15	Sequence 15, Appl
2	530	79.9	146	4 US-08-907-146-15	Sequence 15, Appl
3	496.5	74.9	141	3 US-08-751-359-17	Sequence 17, Appl
4	496.5	74.9	141	4 US-08-907-146-17	Sequence 17, Appl
5	494.5	74.6	147	3 US-08-751-359-18	Sequence 18, Appl
6	494.5	74.6	147	4 US-08-907-146-18	Sequence 18, Appl
7	478.5	72.2	145	3 US-08-751-359-16	Sequence 16, Appl
8	478.5	72.2	145	4 US-08-907-146-16	Sequence 16, Appl
9	444	67.0	120	3 US-08-751-359-25	Sequence 25, Appl
10	444	67.0	120	4 US-08-907-146-25	Sequence 25, Appl
11	393	59.3	127	3 US-09-240-274-27	Sequence 27, Appl
12	390.5	58.9	122	2 US-08-958-201-6	Sequence 6, Appl
13	387.5	58.4	140	3 US-08-983-607-32	Sequence 32, Appl
14	387	58.4	125	2 US-08-428-197-1	Sequence 1, Appl
15	387	58.4	125	5 PCT-US93-10555-1	Sequence 1, Appl
16	386.5	58.3	131	3 US-08-983-607-28	Sequence 28, Appl
17	385.5	58.1	124	3 US-08-983-607-47	Sequence 47, Appl
18	385	58.1	120	2 US-08-428-197-20	Sequence 20, Appl
19	385	58.1	120	2 US-08-428-197-22	Sequence 22, Appl
20	385	58.1	120	2 US-08-428-197-30	Sequence 30, Appl
21	385	58.1	120	2 US-08-428-197-32	Sequence 32, Appl
22	385	58.1	120	5 PCT-US93-10555-20	Sequence 20, Appl
23	385	58.1	120	5 PCT-US93-10555-22	Sequence 22, Appl
24	385	58.1	120	5 PCT-US93-10555-30	Sequence 30, Appl
25	385	58.1	120	5 PCT-US93-10555-32	Sequence 32, Appl
26	383.5	57.8	120	4 US-09-025-769B-38	Sequence 38, Appl
27	383.5	57.8	120	4 US-09-025-769B-63	Sequence 63, Appl

Sequence 178, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 40, Appl
Sequence 53, Appl
Sequence 78, Appl
Sequence 46, Appl
Sequence 1, Appl
Sequence 28, Appl
Sequence 36, Appl
Sequence 104, Appl
Sequence 104, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-751-359-15
; Sequence 15, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-15

Query Match 79.9%; Score 530; DB 3; Length 146;
Best Local Similarity 82.7%; Pred. No. 2.8e-42;
Matches 105; Conservative 2; Mismatches 16; Indels 4; Gaps 1;

QY 1 AVTLDESGGLQTPGGALSLVCKASGTFSSHGMWVROTCKGLWVAGISNTGTYVY 60
|||||
DB 20 AVTLDESGGLQTPGGALSLVCKASGTFSSHGMWVROAPCKGLWVAGIDNTGRYTY 79
|||||

61	APAVKGRATISRNGQSTVBQLNLNLR	RAEDTGTYYCAGGAYCAGCG	----	GDIDAWGHG	116
80	GSAVKGRATISRNGQSTVBQLNLNLR	RAEDTGTYYCAGGAYCAGGAYT	AGSIDAWGHG	139	
117	TEVIVSS	123			
140	TEVIVSS	146			

RESULT 2

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US-08-907-146-15
; Sequence 15, Application US/08907146
; Patent No. 631600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,146

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Query Match	79.9%;	Score 530;	DB 4;	Length 146;
Best Local Similarity	82.7%;	Pred. No. 2.8e-42;		
Matches 105;	Conservative 2;	Mismatches 16;	Indels 4;	Gaps 1;
QY	1	AVLTDESGGGLTPGGALSLVCKASGFTTSSHGMMVROTTPGKGLEWVAGISNTGTYTY	60	
Db	20	AVLTDESGGGLTPGRALSLVCKASGFTTSSYNMGWVRQAPGKGLEFVAGIDNTGRTYGY	79	
QY	61	APAVKGRATISRDNGQSTVRLQLNLNRAEDTGYTCAGKGCAYCAGCG	116	
Db	80	GSAVKGRATISRDNGQSTVRLQLNLNRAEDTGYTCAGKGCAYCAGCG	139	
QY	117	TEVIVSS	123	
Db	140	TEVIVSS	146	

RESULT 3

RESULT 3
US-08-751-359-17

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; Sequence 17, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
;

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Query Match	74.9%	Score 496.5;	DB 3;	Length 141;
Best Local Similarity	81.3%	Pred. No. 3.5e-39;		
Matches 100; Conservative		4; Mismatches 18;	Indels 1;	Gaps 1;

QY	61	APAVKGRATISRDNGOSTVRLQLNNLRAEDTGYTCACKGGAYCAGCGGDIDAWHGTEVI	120
Db	80	GAIVKGRATISRDNGOSTVRLQLNNLRAEDATGYTCACKGRSGFTCVIS-TWVHGTEVI	138
QY	121	VSS 123	
Db	139	VSS 141	

RESULT 4

US-08-07-146-17
Sequence 17, Application US/08097146
Patent No. 6316600
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25

RESULT 6
 US-08-907-146-18
 ; Sequence 18, Application US/08907146
 ; Patent No. 6316600
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael, Nancy M
 ; APPLICANT: Accavitti, Marianne
 ; APPLICANT: Thompson, Craig B
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
 ; ; MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/907,146
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/751,359
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-907-146-18

Query Match 74.6%; Score 494.5; DB 4; Length 147;
Best Local Similarity 78.9%; Pred. No. 5.6e-39;
Matches 101; Conservative 5; Mismatches 17; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 60
Db 20 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 79
QY 61 APAVKGRATISRDNGQSTVRLQNLNLRADTGYTYCAK---GGAYC---ACGGGDDAWGH 115
Db 80 APAVKGRATISRDNGQSTVRLQNLNLRADTGYTYCAKAGSGYCSDDATAGSIDAWGH 139
QY 116 GTEVIVSS 123
Db 140 GTEVIVSS 147

RESULT 7
US-08-751-359-16
; Sequence 16, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08751.359
; FILING DATE: Concurrently Herewith.
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-16

Query Match 72.2%; Score 478.5; DB 3; Length 145;
Best Local Similarity 77.2%; Pred. No. 1.7e-37;
Matches 98; Conservative 6; Mismatches 18; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 60
Db 20 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 78
QY 61 APAVKGRATISRDNGQSTVRLQNLNLRADTGYTYCAK---GGAYCAGCGGDDAWGH 116
Db 79 GAAVKGRATISRDNGQSTVRLQNLNLRADTGYTYCAKESGGSGTSSYAANIDAWGH 138
QY 117 TEVIVSS 123
Db 139 TEVIVSS 145

RESULT 8
US-08-907-146-16
; Sequence 16, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08907.146
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,359
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-907-146-16

Query Match 72.2%; Score 478.5; DB 4; Length 145;
Best Local Similarity 77.2%; Pred. No. 1.7e-37;
Matches 98; Conservative 6; Mismatches 18; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 60
Db 20 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 78
QY 61 APAVKGRATISRDNGQSTVRLQNLNLRADTGYTYCAK---GGAYCAGCGGDDAWGH 116
Db 79 GAAVKGRATISRDNGQSTVRLQNLNLRADTGYTYCAKESGGSGTSSYAANIDAWGH 138

QY 117 TEVIVSS 123
| | | | |
Db 139 TEVIVSS 145

RESULT 9
US-08-751-359-25
; Sequence 25, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-25

Query Match 67.0%; Score 444; DB 3; Length 120;
Best Local Similarity 88.8%; Pred. No. 2.2e-34;
Matches 87; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 1 AVTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYY 60
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Db 20 AVTLDSEGGGLQTPGRALSIVCKASGFTFSSYNNMGWVRQAPGKGLFVAGIDNTGRYTG 79
| | | | |
QY 61 APAVKGRATISRDNGQSVRLQLNLRAEDTGTYYCAK 98
| | | | |
Db 80 GSAVKGRATISRDNGQSVRLQLNLRAEDTGTYYCAK 117
| | | | |

RESULT 10
US-08-907-146-25
; Sequence 25, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,146
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/751,359
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-907-146-25

Query Match 67.0%; Score 444; DB 4; Length 120;
Best Local Similarity 88.8%; Pred. No. 2.2e-34;
Matches 87; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 1 AVTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYY 60
| | | | |
Db 20 AVTLDSEGGGLQTPGRALSIVCKASGFTFSSYNNMGWVRQAPGKGLFVAGIDNTGRYTG 79
| | | | |
QY 61 APAVKGRATISRDNGQSVRLQLNLRAEDTGTYYCAK 98
| | | | |
Db 80 GSAVKGRATISRDNGQSVRLQLNLRAEDTGTYYCAK 117
| | | | |

RESULT 11
US-09-240-274-27
; Sequence 27, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E011s
US-09-240-274-27

Query Match 59.3%; Score 393; DB 3; Length 127;
Best Local Similarity 61.9%; Pred. No. 1.3e-29;

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Matches 78; Conservative 12; Mismatches 32; Indels 4; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGYTYTA 61
Db 2 VQLLESGGLVKPGSLRLSCAASGFTFSSYSMHWVRQAPGKLEWSSISNTYTYTA 61
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAYCAGC----GGDIDAWGHGT 117
Db 62 DAVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDSTRYSNFLWRVRSQGMVWGQGT 121
QY 118 EVIVSS 123
Db 122 TVIVSS 127

RESULT 12
US-08-958-201-6
; Sequence 6, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 2G
; US-08-958-201-6

; Query Match 58.9%; Score 390.5; DB 2; Length 122;
; Best Local Similarity 63.1%; Pred. No. 2.2e-29;
; Matches 77; Conservative 11; Mismatches 33; Indels 1; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGYTYTA 61
Db 2 VNLRESGGLVKPGSLRLSCAASGFTFSDYNSWIRQAPGKLEWVAISGSGNTYTA 61
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAYCAGC----GGDIDAWGHGT 121
Db 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDSTRYSNFLWRVRSQGMVWGQGT 120
QY 122 SS 123
Db 121 SS 122

RESULT 13
US-08-983-607-32
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; Sequence 32, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fuses5 fusion phage construct
; CLONE: V86
; FEATURE:
; NAME/KEY: heavy chain and linker
; US-08-983-607-32

; Query Match 58.4%; Score 387.5; DB 3; Length 140;
; Best Local Similarity 63.7%; Pred. No. 4.8e-29;
; Matches 79; Conservative 12; Mismatches 30; Indels 3; Gaps 2;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGYTYTA 61
Db 2 VQLVQSGGLVQPGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVAISGSGTYTA 61
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGKAYCAGC----IDAWGHGT 119
Db 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDSTRYSNFLWRVRSQGMVWGQGT 120
QY 120 IVSS 123
Db 121 TVSS 124
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RESULT 14
US-08-428-197-1
; Sequence 1, Application US/08428197.
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US93/10555
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 18/2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..125
US-08-428-197-1

Query Match 58.4%; Score 387; DB 2; Length 125;
Best Local Similarity 62.9%; Pred. No. 4.7e-29;
Matches 78; Conservative 10; Mismatches 34; Indels 2; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 2 VQLLESGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWYSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGD--IDAWGHGTEV 119
Db 62 DSVKGRFTISRDNKNTLYQMNSLRADTAIVYCTKGQVLYYGGSGYHWFDPWQGTGLV 121

QY 120 IVSS 123
Db 122 TVSS 125

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Job time : 12.3177 secs

; APPLICANT: SILVERMAN, GREGG J.
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US93/10555
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 18/2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..125
US-08-428-197-1

Query Match 58.4%; Score 387; DB 2; Length 125;
Best Local Similarity 62.9%; Pred. No. 4.7e-29;
Matches 78; Conservative 10; Mismatches 34; Indels 2; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 2 VQLLESGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWYSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGD--IDAWGHGTEV 119
Db 62 DSVKGRFTISRDNKNTLYQMNSLRADTAIVYCTKGQVLYYGGSGYHWFDPWQGTGLV 121

QY 120 IVSS 123
Db 122 TVSS 125

Search completed: September 3, 2003, 12:18:23
Job time : 12.3177 secs

; APPLICANT: SILVERMAN, GREGG J.
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 18/2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..125
PCT-US93-10555-1

Query Match 58.4%; Score 387; DB 5; Length 125;
Best Local Similarity 62.9%; Pred. No. 4.7e-29;
Matches 78; Conservative 10; Mismatches 34; Indels 2; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 2 VQLLESGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWYSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGD--IDAWGHGTEV 119
Db 62 DSVKGRFTISRDNKNTLYQMNSLRADTAIVYCTKGQVLYYGGSGYHWFDPWQGTGLV 121

QY 120 IVSS 123
Db 122 TVSS 125

Search completed: September 3, 2003, 12:18:23
Job time : 12.3177 secs

; APPLICANT: SILVERMAN, GREGG J.
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 18/2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..125
PCT-US93-10555-1

Query Match 58.4%; Score 387; DB 5; Length 125;
Best Local Similarity 62.9%; Pred. No. 4.7e-29;
Matches 78; Conservative 10; Mismatches 34; Indels 2; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 2 VQLLESGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWYSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGD--IDAWGHGTEV 119
Db 62 DSVKGRFTISRDNKNTLYQMNSLRADTAIVYCTKGQVLYYGGSGYHWFDPWQGTGLV 121

QY 120 IVSS 123
Db 122 TVSS 125

Search completed: September 3, 2003, 12:18:23
Job time : 12.3177 secs
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:10:30 ; Search time 22.849 Seconds
(without alignments)
739.130 Million cell updates/sec

Title: US-10-083-424A-18

Perfect score: 663

Sequence: 1 AVTLDESGGGLQTPGGALSL.....AGCGGDIDAWHGTEVIVSS 123

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Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	663	100.0	123	15	US-10-083-424-18
2	508.5	76.7	124	15	US-10-083-424-20
3	494	74.5	127	15	US-10-083-424-38
4	468	70.6	125	15	US-10-083-424-24
5	460.5	69.5	124	15	US-10-083-424-22
6	403.5	60.9	124	15	US-10-040-244-16
7	393.5	59.3	127	11	US-09-848-798-27
8	392.5	59.2	239	11	US-09-880-748-2023
9	390.5	58.9	239	11	US-09-880-748-1105
10	389.5	58.7	239	11	US-09-880-748-2022
11	389.5	58.7	247	11	US-09-880-748-996
12	388.5	58.6	249	11	US-09-880-748-892
13	388.5	58.6	249	11	US-09-880-748-896
14	387.5	58.4	254	11	US-09-880-748-1701
15	387	58.4	248	11	US-09-880-748-913

16	385.5	58.1	118	15	US-10-001-934-39	Sequence 39, Appl
17	385	58.1	123	15	US-10-269-805-59	Sequence 59, Appl
18	384.5	58.0	128	10	US-09-840-459-77	Sequence 77, Appl
19	384.5	58.0	128	10	US-09-840-459-79	Sequence 79, Appl
20	384.5	58.0	254	11	US-09-880-748-1295	Sequence 1295, Ap
21	384	57.9	121	10	US-09-822-698A-3	Sequence 3, Appl
22	384	57.9	381	10	US-09-822-698A-5	Sequence 5, Appl
23	384	57.9	451	10	US-09-822-698A-26	Sequence 26, Appl
24	383.5	57.8	120	14	US-10-025-687-4	Sequence 4, Appl
25	383.5	57.8	120	15	US-10-135-687-4	Sequence 4, Appl
26	383.5	57.8	239	11	US-09-880-748-1922	Sequence 1922, Ap
27	383	57.8	121	10	US-09-840-459-92	Sequence 92, Appl
28	382.5	57.7	124	10	US-09-840-459-89	Sequence 89, Appl
29	382.5	57.7	240	9	US-09-192-854-2	Sequence 2, Appl
30	382.5	57.7	240	10	US-09-968-561A-2	Sequence 2, Appl
31	382.5	57.7	240	12	US-09-968-744A-2	Sequence 2, Appl
32	382	57.6	123	10	US-09-840-459-82	Sequence 82, Appl
33	382	57.6	249	13	US-10-039-785-53	Sequence 53, Appl
34	382	57.6	254	11	US-09-880-748-1139	Sequence 1139, Ap
35	381.5	57.5	249	11	US-09-880-748-512	Sequence 512, App
36	381.5	57.5	249	11	US-09-880-748-1111	Sequence 1111, Ap
37	381	57.5	131	11	US-09-848-798-28	Sequence 28, Appl
38	381	57.5	248	11	US-09-880-748-1876	Sequence 1876, Ap
39	380.5	57.4	223	11	US-09-972-656-86	Sequence 86, Appl
40	380.5	57.4	243	11	US-09-880-748-1935	Sequence 1935, Ap
41	380.5	57.4	249	11	US-09-880-748-397	Sequence 397, App
42	380.5	57.4	249	11	US-09-880-748-911	Sequence 911, App
43	380.5	57.4	249	11	US-09-880-748-1102	Sequence 1102, Ap
44	380.5	57.4	249	11	US-09-880-748-1113	Sequence 1113, Ap
45	380.5	57.4	249	11	US-09-880-748-1115	Sequence 1115, Ap

ALIGNMENTS

RESULT 1
US-10-083-424-18
; Sequence 18, Application US/10083424
; Publication No. US20030104497A1
; GENERAL INFORMATION:
; APPLICANT: Avicore Biotechnology Institute Inc.
; TITLE OF INVENTION: Recombinant Scfv Antibodies Specific to Elmeria spp. Respon
; TITLE OF INVENTION: for Cocciidiosis
; FILE REFERENCE: Avicore-USA-1
; CURRENT APPLICATION NUMBER: US/10/083.424
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: KR 2001-52934
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: chicken hybridoma cell line 2-1
US-10-083-424-18

Query Match	100.0%	Score 663;	DB 15;	Length 123;
Best Local Similarity	100.0%	Pred. No. 7.6e-53;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AVTLDESGGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPCKGLEWVAGISNTGTYTY	60	
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QY	61	APAVKGRATISRDNGQSTVRLQLNLRADTGTYYCAKGGAYCAGCGGDIDAWHGTEVI	120	
Db	61	APAVKGRATISRDNGQSTVRLQLNLRADTGTYYCAKGGAYCAGCGGDIDAWHGTEVI	120	
QY	121	VSS 123		
Db	121	VSS 123		

Query Match	69.5%;	Score 460.5;	DB 15;	Length 124;
Best local Similarity	75.0%;	Pred. No. 1.6e-34;		
Matches	93;	Conservative 7;	Mismatches 23;	Indels 1; Gaps 1;

QY	1	AVTLDESGGGLQTPGGALSIVCKASGFTFSHGMMVWROP	PGKLEWVAGI-SNTIGTYY	59
Db	1	AVTLDESGGGLQTPGGGLSLVCKSGGLDFSSYAMGVWVQAP	PGKLEFVAGIKKNDGSWTN	60
QY	60	YAPAVGRATISRDNGQSTVRLQNLNLRADTGTYYCAKGGAYC	ACGGGDIDAWHGTEV	119
Db	61	YAPAVGRATISRDNGQSTVRLQNLNLRADTGTYYCTD	VNSGYDPAADIDAWHGTEV	120

Search completed: September 3, 2003, 12:53:14
Job time : 23.849 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:09:30 ; Search time 198.914 Seconds
(without alignments)
538.192 Million cell updates/sec

Title: US-10-083-424A-18

Perfect score: 663

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	663	100.0	123	26	US-10-083-424-18
2	663	100.0	123	26	US-10-083-424A-18

Sequence 18, Appl
Sequence 18, Appl

3	541	81.6	585	22	US-09-791-537-4487	Sequence 4487, Ap
4	541	81.6	585	22	US-09-791-537-63314	Sequence 63314, A
5	538	81.1	250	22	US-09-791-537-130345	Sequence 130345, A
6	537	81.0	236	22	US-09-791-537-129947	Sequence 129947, A
7	534	80.5	235	22	US-09-791-537-129977	Sequence 129977, A
8	534	80.5	237	22	US-09-791-537-129974	Sequence 129974, A
9	534	80.5	248	22	US-09-791-537-130354	Sequence 130354, A
10	527	79.5	242	22	US-09-791-537-130363	Sequence 130363, A
11	525	79.2	245	22	US-09-791-537-139118	Sequence 139118, A
12	524.5	79.1	258	1	PCT-US02-29003A-55	Sequence 55, Appl
13	524.5	79.1	258	1	PCT-US02-29003B-55	Sequence 55, Appl
14	522	78.7	138	22	US-09-791-537-44408	Sequence 44408, A
15	521.5	78.7	234	22	US-09-791-537-129944	Sequence 129944, A
16	521	78.6	124	22	US-09-791-537-129879	Sequence 129879, A
17	519.5	78.4	123	22	US-09-791-537-129857	Sequence 129857, A
18	519	78.3	234	22	US-09-791-537-133373	Sequence 133373, A
19	516.5	77.9	126	22	US-09-791-537-68235	Sequence 68235, A
20	515.5	77.8	122	22	US-09-791-537-129900	Sequence 129900, A
21	515	77.7	246	22	US-09-791-537-130347	Sequence 130347, A
22	515	77.7	252	1	PCT-US02-29003A-58	Sequence 58, Appl
23	515	77.7	252	1	PCT-US02-29003B-58	Sequence 58, Appl
24	513	77.4	250	1	PCT-US02-29003A-60	Sequence 60, Appl
25	513	77.4	250	1	PCT-US02-29003B-60	Sequence 60, Appl
26	510	76.9	231	22	US-09-791-537-135106	Sequence 135106, A
27	510	76.9	244	22	US-09-791-537-130346	Sequence 130346, A
28	510	76.9	244	22	US-09-791-537-130378	Sequence 130378, A
29	509	76.8	121	22	US-09-791-537-129880	Sequence 129880, A
30	508.5	76.7	124	26	US-10-083-424-20	Sequence 20, Appl
31	508.5	76.7	124	26	US-10-083-424A-20	Sequence 20, Appl
32	506.5	76.4	233	22	US-09-791-537-129946	Sequence 129946, A
33	506	76.3	234	22	US-09-791-537-130343	Sequence 130343, A
34	505.5	76.2	124	22	US-09-791-537-129918	Sequence 129918, A
35	503	75.9	244	22	US-09-791-537-130380	Sequence 130380, A
36	502	75.7	131	22	US-09-791-537-71539	Sequence 71539, A
37	501.5	75.6	254	1	PCT-US02-29003A-56	Sequence 56, Appl
38	501.5	75.6	254	1	PCT-US02-29003B-56	Sequence 56, Appl
39	500.5	75.5	120	22	US-09-791-537-71513	Sequence 71513, A
40	500.5	75.5	128	22	US-09-791-537-68204	Sequence 68204, A
41	500.5	75.5	132	22	US-09-791-537-68219	Sequence 68219, A
42	500.5	75.5	250	1	PCT-US02-29003A-54	Sequence 54, Appl
43	500.5	75.5	250	1	PCT-US02-29003A-62	Sequence 62, Appl
44	500.5	75.5	250	1	PCT-US02-29003B-54	Sequence 54, Appl
45	500.5	75.5	250	1	PCT-US02-29003B-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-083-424-18
; Sequence 18, Application US/10083424
; GENERAL INFORMATION:
; APPLICANT: Avicore Biotechnology Institute Inc.
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Response
; FILE REFERENCE: Avicore-USA-1
; TITLE OF INVENTION: for Coccidiosis
; FILE REFERENCE: Avicore-USA-1
; CURRENT APPLICATION NUMBER: US/10/083,424
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: KR 2001-52934
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Knapten 1.71
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: chicken hybridoma cell line 2-1
US-10-083-424-18

Query Match 100.0%; Score 663; DB 26; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVTLDESGGLQTPGGALSLVCKASGFTSSHHMMVVRQTPGKGLWVAGISNIGTGYTY 60

Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60
61 APVKGRTATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120
61 APVKGRTATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120
QY 121 VSS 123
121 VSS 123
Db 121 VSS 123

RESULT 2

US-10-083-424A-18
; Sequence 18, Application US/10083424A
; GENERAL INFORMATION:
; APPLICANT: Avicore Biotechnology Institute Inc.
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Responsible
; FILE REFERENCE: Avicore-USA-1
; CURRENT APPLICATION NUMBER: US/10/083.424A
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: KR 2001-52934
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: chicken hybridoma cell line 2-1
US-10-083-424A-18

Query Match 100.0%; Score 663; DB 26; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60
Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60
QY 61 APVKGRTATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120
Db 61 APVKGRTATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120
QY 121 VSS 123
Db 121 VSS 123

RESULT 3

US-09-791-537-4487
; Sequence 4487, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4487
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-791-537-4487

Query Match 81.6%; Score 541; DB 22; Length 585;
Best Local Similarity 82.9%; Pred. No. 1.2e-43;
Matches 102; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60
Db 20 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 79
QY 61 APVKGRTATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120
Db 80 GPAVQGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 139
QY 121 VSS 123
Db 140 VSS 142

RESULT 4

US-09-791-537-63314
; Sequence 63314, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63314
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-791-537-63314

Query Match 81.6%; Score 541; DB 22; Length 585;
Best Local Similarity 82.9%; Pred. No. 1.2e-43;
Matches 102; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60
Db 20 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 79
QY 61 APVKGRTATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120
Db 80 GPAVQGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGIDAWHGTEVI 139
QY 121 VSS 123
Db 140 VSS 142

RESULT 5

US-09-791-537-130345
; Sequence 130345, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130345
; LENGTH: 250
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-130345

Query Match 81.1%; Score 538; DB 22; Length 250;
Best Local Similarity 83.5%; Pred. No. 9.2e-44;
Matches 106; Conservative 3; Mismatches 14; Indels 4; Gaps 2;

Best Local Similarity 82.7%; Pred. No. 2.2e-43;
Matches 105; Conservative 3; Mismatches 15; Indels 4; Gaps 2;
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60
Db 122 AVTLDESGGLQTPGGTSLVCKASGFTFSSFMVVRQAPGKLEWVGQITYSGRYTSY 181
QY 61 APAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAKGG-AYC---ACGGGDIDAWGHG 116
Db 182 APAVKGRATISRDNQSTVRLQLNNLRAEDTATYYCAKGSYCNTRGRCVGTIDAWGHG 241
QY 117 TEVIVSS 123
Db 242 TEVIVSS 248

RESULT 10
US-09-791-537-130363
; Sequence 130363, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130363
; LENGTH: 242
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-130363

Query Match 79.5%; Score 527; DB 22; Length 242;
Best Local Similarity 82.8%; Pred. No. 1e-42;
Matches 106; Conservative 2; Mismatches 10; Indels 10; Gaps 2;
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Db 120 AVTLDESGGLQTPGGALSLVCKASGFTFSSYGMVVRQAPGKLELIASISKTGYTY 179
QY 61 APAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAKGGAYCAGCG-----GDIDAWGH 115
Db 180 GSAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAK-----ACGYSYETGCDIDAWGH 234
QY 116 TEVIVSS 123
Db 235 TEVIVSS 242

RESULT 11
US-09-791-537-139118
; Sequence 139118, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139118
; LENGTH: 245
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-139118

Query Match 79.2%; Score 525; DB 22; Length 245;
Best Local Similarity 82.5%; Pred. No. 1.7e-42;
Matches 104; Conservative 6; Mismatches 10; Indels 6; Gaps 2;
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60
Db 123 AVTLDESGGLQTPGGALSLVCKASGFTFSSYGMVVRQAPGKLEVVASISKTGYTY 182
QY 61 APAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAK---GGAYCAGCGDDIDAWGHGT 117
Db 183 GSAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAKPGACGHSYDSC---LDAWGHGT 239
QY 118 EVIVSS 123
Db 240 EVIVSS 245

RESULT 12
PCT-US02-29003A-55
; Sequence 55, Application PC/TUS0229003A
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten
; APPLICANT: Forschung e.V.
; APPLICANT: ZHANG, Mei Yun
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: ZIMMERMANN, Sabine
; APPLICANT: DI FIORE, Stefano
; APPLICANT: EMANS, Neil
; APPLICANT: FISCHER, Rainer
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Met
; TITLE OF INVENTION: of Making and Using
; FILE REFERENCE: FRAU-202.1PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29003A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/318,904
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ScFv P6
PCT-US02-29003A-55

Query Match 79.1%; Score 524.5; DB 1; Length 258;
Best Local Similarity 82.0%; Pred. No. 2e-42; Mismatches 16; Indels 5; Gaps 3;
Matches 105; Conservative 2; Mismatches 16; Indels 5; Gaps 3;
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60
Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSYGMVVRQAPGKLEWVAGIDAGIYTY 60
QY 61 APAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAKGG-AYC---ACGGGD-IDAWGH 115
Db 61 GAAVKGRATISRDNQSTVRLQLNNLRAEDTGYTYCAKGGAYCDSGTWCADDYDIDAWGH 120
QY 116 GTEVIVSS 123
Db 121 GTEVIVSS 128

RESULT 13
PCT-US02-29003B-55
; Sequence 55, Application PC/TUS0229003B
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten
; APPLICANT: Forschung e.V.
; APPLICANT: ZHANG, Mei Yun
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: ZIMMERMANN, Sabine
; APPLICANT: DI FIORE, Stefano

; APPLICANT: EMANS, Neil
; APPLICANT: FISCHER, Rainer
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods
; FILE REFERENCE: FRAU-202.1PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29003B
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/318,904
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ScFv P6
PCT-US02-29003B-55

Query Match 79.1%; Score 524.5; DB 1; Length 258;
Best Local Similarity 82.0%; Pred. No. 2e-42;
Matches 105; Conservative 2; Mismatches 16; Indels 5; Gaps 3;
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60
Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQAPGKLEWVAGIDADGIYTN 60
QY 61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYTYCAKGG-AYC---AGCGGD-IDAWGH 115
Db 61 GAAVKGGRATISRDNQSTVRLQNLNLRADTGTYTYCAKGGAYGYCDSTWCADDYIDAWGH 120
QY 116 GPEVTVSS 123
Db 121 GPEVTVSS 128

RESULT 14
US-09-791-537-44408
; Sequence 4408, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44408
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-791-537-44408

Query Match 78.7%; Score 522; DB 22; Length 138;
Best Local Similarity 84.6%; Pred. No. 1.7e-42;
Matches 104; Conservative 2; Mismatches 13; Indels 4; Gaps 1;
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60
Db 20 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQAPGKLEWVAGIDNTGRVTGY 79
QY 61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYTYCAKGGAYCAGCGGDDAWGHGTEVI 120
Db 80 GSAVKGGRATISRDNQSTVRLQNLNLRADTGTYTYCAK-----AAGTAGSIDAWGHGTEVI 135
QY 121 VSS 123
Db 136 VSS 138

RESULT 15

US-09-791-537-129944
; Sequence 129944, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129944
; LENGTH: 234
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-129944

Query Match 78.7%; Score 521.5; DB 22; Length 234;
Best Local Similarity 83.7%; Pred. No. 3.5e-42;
Matches 103; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTYA 61
Db 112 VMLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQAPGKLEWVAVISNTGSGTYTG 171
QY 62 PAYKGRATISRDNQSTVRLQNLNLRADTGTYTYCAKGGAYC-ACGCGDIDAWGHGTEVI 120
Db 172 SAYKGRATISRDNQSTVRLQNLNLRADTGTYTYCAKRGTCYNGTCIDAWGHGTEVI 231
QY 121 VSS 123
Db 232 VSS 234

Search completed: September 3, 2003, 12:49:33
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